
M P E R E H

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MPsrch.p protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:51:23 1998; MasPar time 9.06 Seconds
664.722 Million cell updates/sec

Tabular output not generated.

Title: >US-08-765-588-8
Description: (1-143) from US08765588.pep
Perfect Score: 1078
Sequence: 1 MSPILRLLLAALLQAPAQ.....CRPKKDSAVKPRCKRLR 143

Scoring table: PAM 150
Gap 11

Searched: 140555 segs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: splrembl6
1:sp.fungi 2:sp.human 3:sp.invertebrate 4:sp.mammal
5:sp.mhc 6:sp.organelle 7:sp.phase 8:sp.plant
9:sp.bacteria 10:sp.rodent 11:sp.virus 12:sp.vertebrate
13:sp.unclassified

Statistics: Mean 40.352; Variance 65.917; scale 0.612

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

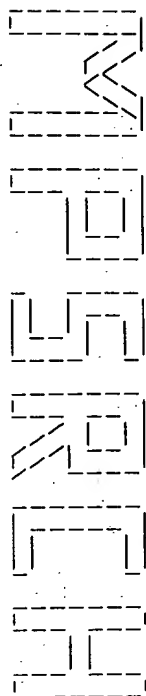
SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1023	94.9	207	2	Q16528	VEGF RELATED FACTOR IS 1.25e-224
2	947	87.8	207	10	Q64290	VASCULAR ENDOTHELIAL G 3.22e-205
3	620	57.5	116	10	Q35485	VASCULAR ENDOTHELIAL G 1.25e-122
4	395	36.6	148	12	Q42571	VASCULAR ENDOTHELIAL G 1.95e-67
5	373	34.6	232	2	Q16889	VASCULAR ENDOTHELIAL G 3.57e-62
6	369	34.2	194	12	Q42572	VASCULAR ENDOTHELIAL G 3.20e-61
7	333	30.9	216	12	Q91420	VASCULAR ENDOTHELIAL G 1.06e-52
8	278	25.8	75	4	Q18843	VASCULAR ENDOTHELIAL G 6.32e-40
9	275	25.5	158	10	Q63434	PLACENTA GROWTH FACTOR 3.07e-39
10	199	18.4	358	10	P97946	VASCULAR ENDOTHELIAL G 4.03e-22
11	192	17.8	326	10	Q35251	VASCULAR ENDOTHELIAL G 7.71e-21
12	176	16.3	415	10	P97953	VASCULAR ENDOTHELIAL G 1.80e-17
13	170	15.8	185	2	Q15354	C-SIS PROTO-ONCOGENE (3.14e-16
14	170	15.8	271	11	Q41283	POLYPROTEIN PRECURSOR 8.10e-16
15	168	15.6	210	4	Q29613	C-SIS ONCOGENE (PLATEL 4.18e-06
16	147	13.6	183	10	Q63740	PDGF PROTEIN (FRAGMENT 4.18e-06
17	118	10.9	126	10	Q35757	VASCULAR ENDOTHELIAL G 1.71e-02
18	97	9.0	952	9	Q32915	GLYCINE DEHYDROGENASE 7.48e-02
19	93	8.6	411	8	Q38946	GLUTAMATE DEHYDROGENAS 3.15e-01
20	89	8.3	571	9	Q51763	IS1162 DNA.

21	87	8.1	411	8	Q04937	NADH GLUTAMATE DEHYDRO 6.35e-01
22	86	8.0	394	9	P96447	EXP6. 8.98e-01
23	86	8.0	605	2	Q00304	VOLTAGE-DEPENDENT CALC 8.98e-01
24	85	7.9	411	8	Q04871	GLUTAMATE DEHYDROGENS 1.27e+00
25	85	7.9	411	8	Q43260	GLUTAMATE DEHYDROGENS 1.27e+00
26	85	7.9	411	8	Q04872	GLUTAMATE DEHYDROGENS 1.27e+00
27	85	7.9	412	8	P93541	GLUTAMATE DEHYDROGENS 1.27e+00
28	85	7.9	423	10	P97569	KALLISTATIN. 1.27e+00
29	84	7.8	641	10	Q08463	FRITZLED PROTEIN HOMOL 1.78e+00
30	83	7.7	393	9	Q46412	MAJOR OUTER MEMBRANE P 2.49e+00
31	83	7.7	393	9	Q46413	(INDIVIDUAL ISOLATE 11 2.49e+00
32	83	7.7	393	9	Q46411	(INDIVIDUAL ISOLATE 98 2.49e+00
33	83	7.7	393	9	Q46414	MAJOR OUTER MEMBRANE P 2.49e+00
34	83	7.7	393	9	Q46415	MAJOR OUTER MEMBRANE P 2.49e+00
35	83	7.7	393	9	Q46410	MAJOR OUTER MEMBRANE P 2.49e+00
36	83	7.7	393	9	Q46409	MAJOR OUTER MEMBRANE P 2.49e+00
37	83	7.7	394	9	Q06020	MAJOR OUTER MEMBRANE P 2.49e+00
38	83	7.7	394	9	Q46408	MAJOR OUTER MEMBRANE P 2.49e+00
39	83	7.7	396	9	Q46406	MAJOR OUTER MEMBRANE P 2.49e+00
40	83	7.7	722	3	Q19738	F22E12.1 (FRAGMENT). 2.49e+00
41	83	7.7	1031	3	Q09489	ORGANELLE-TYPE CALCIUM 2.49e+00
42	83	7.7	4096	2	Q13327	DNA DEPENDENT PROTEIN 2.49e+00
43	83	7.7	4127	2	P78527	DNA-DEPENDENT PROTEIN 2.49e+00
44	82	7.6	488	11	Q03822	ENV POLYPROTEIN (CONTA 3.48e+00
45	82	7.6	619	10	Q62309	TESTIS NUCLEAR RNA-BIN 3.48e+00

ALIGNMENTS

RESULT ID	1	PRELIMINARY; PRT;	207 AA.
AC	Q16528;		
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)		
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)		
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)		
DE	VEGF RELATED FACTOR ISOFORM VRF186 PRECURSOR.		
GN	VRF OR VEGF-B.		
OS	HOMO SAPIENS (HUMAN).		
CC	EMBAROTIA; METACOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; PRIMATES.		
CC	[1]		
RN	SEQUENCE FROM N.A.		
RP	TISSUE-BRAIN;		
RA	GRIMOND S., LAGERBRANTZ J., DRINKATER C., STILINS G., TOWNSON S., POLLOCK P., COTLEY D., CARSON E., RAKAR S., NORDENSKOLD K., WARD L., HAYWARD N., WEBER G., GENOME RES. 6:122-129(1996).		
RL	[2]		
RN	SEQUENCE FROM N.A.		
RP	TISSUE-FIBROSARCOMA HT-1080;		
RA	MEDLINE; 96197355.		
RA	OLOFSSON B.,		
RL	PROC. NATL. ACAD. SCI. U.S.A. 93:2576-2581(1996).		
RN	[3]		
RN	SEQUENCE FROM N.A.		
RP	TISSUE-FIBROSARCOMA HT-1080;		
RA	MEDLINE; 96325041.		
RA	OLOFSSON B., PAUSOLA K., VON EULER G., CHILOV D., ALITALO K., ERIKSSON U., J. BIOL. CHEM. 271:19310-19317(1996).		
DR	EMBL; U43368; G1216396; -		
DR	EMBL; U52819; G1488259; -		
DR	PROSITE; P500248; PDGF. 1.		
KW	SIGNAL.		
FT	CHAIN	1	21
FT	CHAIN	22	207
SQ	SEQUENCE	207 AA; 21602 MW; 16BDF6F1 CAC32;	
Query Match	94.9%;	Score 1023;	DB 2; Length 207;
Best Local Similarity	100.0%;	Pred. No. 1.25e-224;	
Matches	177;	Conservative 0;	Mismatches 0; Gaps 0;
Db	1 MSPILRLLLAALLQAPAQVSPDAPGHRVVSMDVYTATGCPREVVPLVEL 60		



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MPsrch.p protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Sep 18 13:50:48 1998; MasPar time 5.20 Seconds
Tabular output not generated. 689.290 Million cell updates/sec

Title: >US-08-765-588-8
Description: (1-143) from US08765588.pep
Perfect Score: 1078
Sequence: 1 MSPILRLILALLQAPAQ.....CRPKKDSAVKPDCKRLRR 143

Scoring table:
PAM 150
Gap 11

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 42.257; Variance 63.671; scale 0.664

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1023	94.9	188	1	VEGF_HUMAN VASCULAR ENDOTHELIAL G	3.01e-242
2	947	87.8	188	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	3.02e-221
3	383	35.5	146	1	VEGF_SHEEP VASCULAR ENDOTHELIAL G	2.76e-67
4	375	34.8	190	1	VEGF_RAT VASCULAR ENDOTHELIAL G	1.03e-66
5	373	34.6	215	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	1.03e-66
6	371	34.4	190	1	VEGF_HUMAN VASCULAR ENDOTHELIAL G	3.37e-66
7	371	34.4	190	1	VEGF_BOVIN VASCULAR ENDOTHELIAL G	1.16e-64
8	365	33.9	190	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	7.56e-62
9	354	32.8	144	1	VEGF_CANARO VASCULAR ENDOTHELIAL G	1.82e-50
10	309	28.7	170	1	PLGF_HUMAN PLACENTA GROWTH FACTOR	9.45e-44
11	303	28.1	133	1	VEGF_ORN2 VASCULAR ENDOTHELIAL G	5.77e-49
12	282	26.2	158	1	PLGF_MOUSE PLACENTA GROWTH FACTOR	2.48e-39
13	264	24.5	148	1	VEGF_COTJA VASCULAR ENDOTHELIAL G	1.81e-18
14	175	16.2	419	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	3.02e-18
15	174	16.1	148	1	VEGF_OPEN7 VASCULAR ENDOTHELIAL G	3.02e-18
16	174	16.1	223	1	PDGF_RAT PLATELET-DERIVED GROWT	1.39e-17
17	171	15.9	213	1	PDGF_RABIT PLATELET-DERIVED GROWT	2.31e-17
18	170	15.8	226	1	TSIS_HUMAN PDGF-RELATED TRANSFORM	6.34e-17
19	170	15.8	241	1	PDGF_HUMAN PLATELET-DERIVED GROWT	6.34e-17
20	168	15.6	241	1	PDGF_MOUSE PLATELET-DERIVED GROWT	2.87e-16
21	168	15.6	245	1	PDGF_FELCA PLATELET-DERIVED GROWT	4.74e-16
22	165	15.3	211	1	PDGF_MOUSE PLATELET-DERIVED GROWT	4.74e-16
23	164	15.2	204	1	PDGF_RAT PLATELET-DERIVED GROWT	4.74e-16

24	164	15.2	211	1	PDGF_HUMAN PLATELET-DERIVED GROWT	4.74e-16
25	163	15.1	226	1	PDGF_XENIA PLATELET-DERIVED GROWT	7.81e-16
26	157	14.6	241	1	PDGF_SHEEP PLATELET-DERIVED GROWT	1.54e-14
27	91	8.4	411	1	DHE3_VITVI GLUTAMATE DEHYDROGENAS	8.40e-02
28	91	8.4	493	1	ACHE_HUMAN ACETYLCHOLINE RECEPTOR	8.40e-02
29	90	8.3	539	1	LIT4_CABEL LIN-14 PROTEIN.	1.22e-01
30	88	8.2	598	1	CYSJ_SALTY SULFITE REDUCTASE (NAD	2.55e-01
31	87	8.1	411	1	LYOX_MOUSE PROTEIN-LYSINE 6-OXIDA	3.67e-01
32	86	8.0	567	1	CCB2_MOUSE DIHYDROPYRIDINE-SENSIT	5.26e-01
33	86	8.0	649	1	YAV3_SCHPO HYDROTICAL 74.5 KD P	5.26e-01
34	85	7.9	60	1	MT3_PICGL METALLOTHIONEIN-LIKE P	7.51e-01
35	84	7.8	916	1	SCRB_LIMPO BETA SCRUTIN.	1.07e+00
36	84	7.8	941	1	GCSP_MYCTU PROBABLE GLYCINE DEHYD	1.07e+00
37	83	7.7	174	1	Y119_HUMAN HYPOTHEICAL Y-CHROMOS	1.52e+00
38	83	7.7	393	1	OMPL_CHLTR MAJOR OUTER MEMBRANE P	1.52e+00
39	83	7.7	394	1	OMPB_CHLTR MAJOR OUTER MEMBRANE P	1.52e+00
40	83	7.7	395	1	OMPF_CHLTR MAJOR OUTER MEMBRANE P	1.52e+00
41	83	7.7	396	1	OMPA_CHLTR MAJOR OUTER MEMBRANE P	1.52e+00
42	83	7.7	397	1	OMPN_CHLTR MAJOR OUTER MEMBRANE P	1.52e+00
43	83	7.7	399	1	P2X1_RAT P2X PURINOCCEPTOR 1 (AT	1.52e+00
44	83	7.7	601	1	PM1L_DROME NUBBIN PROTEIN (TWIN	1.52e+00
45	83	7.7	1110	1	VGLM_INSV M POLYPROTEIN PRECURSO	1.52e+00

ALIGNMENTS

RESULT	ID	VEGF_HUMAN	STANDARD	PRT	168 AA.
AC	P49765	01-OCT-1996 (REL. 34, CREATED)			
DT	01-OCT-1996	(REL. 34, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997	(REL. 35, LAST ANNOTATION UPDATE)			
DE	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR).				
GN	VEGF OR VRF.				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
CC	EUTHERIA; PRIMATES.				
CC	[1]				
CC	SEQUENCE FROM N.A.				
CC	MEDLINE; 96197355.				
CC	OLOFFSON B., PAJUSOLA K., KAIRAINEN A., VON EULER G., JOKROV V.,				
CC	RA SASELA O., ORPANA A., PETERSSON R.F., ALTALIO K., ERIKSSON U.,				
CC	PROC. NATL. ACAD. SCI. U.S.A. 93:2576-2581(1996).				
CC	[2]				
CC	SEQUENCE FROM N.A.				
CC	GRIMMOND S., LAGERCRANTZ J., DRINKWATER C., SILINS G., TOWNSON S.,				
CC	RA POLLOCK P., GOTLEY D., CARSON E., RAKAR S., NORDENSKJOLD M.,				
CC	RA GENOME RES. 6:122-129(1996).				
CC	-1- FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BINDS HEPARIN.				
CC	-1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED. CAN ALSO FORM HETERODIMER WITH VEGF.				
CC	-1- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN.				
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXCEPT LIVER.				
CC	-1- HIGHEST LEVELS FOUND IN HEART, SKELETAL MUSCLE AND PANCREAS.				
CC	-1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.				
CC	EMBL; U48801; G1334823; -				
CC	EMBL; U43369; G1216398; -				
CC	DR MIM; 601398; -				
CC	DR PROSITE; PS00249; PDGF; 1.				
CC	DR MITOGEN. GROWTH FACTOR; SIGNAL; HEPARIN-BINDING.				
CC	FT SIGNAL. 1				
CC	FT CHAIN. 22				
CC	FT SEQUENCE. 188 AA; 21261 MW; 35EA8904 CRC32;				
SO	VEGF_HUMAN				
SO	VEGF_MOUSE				
SO	VEGF_SHEEP				
SO	VEGF_RAT				
SO	VEGF_MOUSE				
SO	VEGF_BOVIN				
SO	VEGF_MOUSE				
SO	VEGF_CANARO				
SO	PLGF_HUMAN				
SO	VEGF_ORN2				
SO	PLGF_MOUSE				
SO	VEGF_COTJA				
SO	VEGF_MOUSE				
SO	VEGF_OPEN7				
SO	PDGF_RAT				
SO	PDGF_RABIT				
SO	TSIS_HUMAN				
SO	PDGF_HUMAN				
SO	PDGF_MOUSE				
SO	PDGF_FELCA				
SO	PDGF_MOUSE				
SO	PDGF_RAT				

Query Match: 94.9%; Score 1023; DB 1; Length 188;
Best Local Similarity: 97.9%; Pred. No. 3.01e-242;
Matches: 138; Conservative: 0; Mismatches: 3; Indels: 0; Gaps: 0;

M P O E R E H
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MSPRCH_PP protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Sep 18 13:49:30 1998; MasPar time 7.64 Seconds
Tabular output not generated. 684.018 Million cell updates/sec

Title: >US-08-765-588-8
Description: (1-143) from US08765588.pep
Perfect Score: 1078
Sequence: 1 MSPRLRLRLAALQLAPAQ.....CRPKKDSAVKPDRCRLRR 143

Scoring table:
PAM 150
Gap 11

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

plrs5
1:plrl 2:plrl 3:plrl 4:plrl 5:nrl3d

Statistics: Mean 40.311; Variance 76.368; scale 0.528

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	947	87.8	188	2	JC4680	9.64e-177
2	947	87.8	207	2	JC4679	9.64e-177
3	383	35.5	146	2	S57956	2.14e-95
4	375	34.8	120	2	A33787	9.54e-54
5	375	34.8	190	2	A33987	9.54e-54
6	373	34.6	214	2	A44881	2.46e-53
7	373	34.6	232	2	A44551	2.46e-53
8	371	34.4	190	2	S52130	6.35e-53
9	371	34.4	190	2	B44881	6.35e-53
10	365	33.9	190	2	B40080	6.35e-53
11	318	29.5	143	2	A41236	1.09e-42
12	302	28.0	133	2	B49530	4.01e-42
13	275	25.5	158	2	A56125	6.60e-39
14	264	24.5	128	2	I51295	1.55e-33
15	175	16.2	419	2	S69207	2.37e-31
16	174	16.1	448	2	D49530	1.50e-14
17	174	16.1	225	2	S25097	2.26e-14
18	171	15.9	166	2	JN0248	7.79e-14
19	171	15.9	198	2	JN0735	7.79e-14
20	170	15.8	161	2	I38108	1.17e-13
21	170	15.8	185	2	S58383	1.17e-13
22	170	15.8	226	1	TWAVSS	1.17e-13
23	170	15.8	230	2	A5030	1.17e-13

ENTRY	1	JC4680	#type complete	platelet-derived growth factor-related factor 167 - mouse
TITLE		VWF 167 protein		
ALTERNATE_NAMES				
ORGANISM		Human		
DATE		10-May-1996		
ACCESSIONS		JC4680		
REFERENCE		Townson, S.; Lagercrantz, J.; Grimmond, S.; Sillins, G.; Nordenskiold, M.; Weber, G.; Hayward, N. Blochem. Biophys. Res. Commun. (1996) 220:922-928		
#authors		1		
#journal		1		
#title		1		
#accession		JC4680		
#molecule_type		mRNA		
#residues		188		
#cross-references		GB:U43837; NID:G1314335; PID:G1314336		
COMMENT		This factor is a mitogen, that is selective for endothelial cells, and belongs to a family of growth factor. This transcript is differentially spliced to produce two major isoforms, vascular endothelial growth factors 167 and VEGF 186.		

ALIGNMENTS

ENTRY	1	JC4680	#type complete	platelet-derived growth factor-related factor 167 - mouse
TITLE		VWF 167 protein		
ALTERNATE_NAMES				
ORGANISM		Human		
DATE		10-May-1996		
ACCESSIONS		JC4680		
REFERENCE		Townson, S.; Lagercrantz, J.; Grimmond, S.; Sillins, G.; Nordenskiold, M.; Weber, G.; Hayward, N. Blochem. Biophys. Res. Commun. (1996) 220:922-928		
#authors		1		
#journal		1		
#title		1		
#accession		JC4680		
#molecule_type		mRNA		
#residues		188		
#cross-references		GB:U43837; NID:G1314335; PID:G1314336		
COMMENT		This factor is a mitogen, that is selective for endothelial cells, and belongs to a family of growth factor. This transcript is differentially spliced to produce two major isoforms, vascular endothelial growth factors 167 and VEGF 186.		

GENETICS

#gene	1	JC4680	#type complete	platelet-derived growth factor-related factor 167 - mouse
#map_position		13772		
#introns		1		
FEATURE		1-21		
22-188				

SUMMARY

Query Match	87.8%	Score 947	DB 2	Length 188
Best local similarity	87.2%	Pred. No. 9.64e-177		
Matches	123	Conservative	10	Mismatches 8; Indels 0; Gaps 0;

DB	1	MSPRLRLRLAALQLAPAQVQFQSPHQKRVVWIDYVARATQPREVVPPLSMET 60
QY	1	MSPRLRLRLAALQLAPAQVQFQSPHQKRVVWIDYVARATQPREVVPPLSMET 60
DB	61	MGNVYKQVPSCTVQRCGGCCPDGECVPTGQHQVQRMQIMIQVSSQIGKSLSEHS 120
QY	61	MGNVYKQVPSCTVQRCGGCCPDGECVPTGQHQVQRMQIMIQVSSQIGKSLSEHS 120
DB	121	OCCEPRPKKDSAVKPDRCRL 141
QY	121	OCCEPRPKKDSAVKPDRCRL 141

M P O S E R E L I
(TM)

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MPsrch.p protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:53:16 1998; Maspar time 9.07 seconds

Tabular output not generated. 498,946 Million cell updates/sec

Title: >US-08-765-588-8
Description: (1-143) from US08765588.pep
Perfect Score: 1078
Sequence: 1 MSPRLRLALALQLAPAQ.....CRPKKDSAVKPRCKRLRR 143

Scoring table: PAM 150
Gap 11

Searched: 288199 segs, 31643258 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

a-pending
1: P9 2: U60 3: U7 4: U80 5: U81 6: U82 7: U83 8: U84 9: U85
10: U86 11: U87 12: U88 13: U89 14: U90 15: U91 16: NEM7
17: NEM6 18: NEM7 19: NEM8 20: NEM9

Statistics: Mean 29.808; Variance 121.862; scale 0.245

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1023	94.9	188	9	US- Sequence 11, Applicati	6.14e-92
2	1023	94.9	188	10	US- Sequence 11, Applicati	6.14e-92
3	1023	94.9	188	10	US- Sequence 11, Applicati	6.14e-92
4	1023	94.9	188	8	US- Sequence 11, Applicati	6.14e-92
5	1023	94.9	188	11	US- Sequence 57, Applicati	6.14e-92
6	1023	94.9	188	10	US- Sequence 56, Applicati	6.14e-92
7	1023	94.9	188	9	US- Sequence 11, Applicati	6.14e-92
8	1023	94.9	188	9	US- Sequence 11, Applicati	6.14e-92
9	1023	94.9	207	10	US- Sequence 15, Applicati	6.14e-92
10	1023	94.9	207	10	US- Sequence 15, Applicati	6.14e-92
11	1023	94.9	207	9	US- Sequence 15, Applicati	6.14e-92
12	1023	94.9	207	10	US- Sequence 15, Applicati	6.14e-92
13	1023	94.9	207	9	US- Sequence 15, Applicati	6.14e-92
14	1005	93.2	206	12	US- Sequence 2, Applicatio	4.49e-90
15	950	88.1	188	12	US- Sequence 1, Applicatio	2.19e-84
16	947	87.8	188	8	US- Sequence 5, Applicatio	4.48e-84
17	947	87.8	188	10	US- Sequence 5, Applicatio	4.48e-84
18	947	87.8	188	8	US- Sequence 5, Applicatio	4.48e-84
19	947	87.8	188	9	US- Sequence 5, Applicatio	4.48e-84
20	947	87.8	188	9	US- Sequence 5, Applicatio	4.48e-84
21	947	87.8	188	9	US- Sequence 5, Applicatio	4.48e-84

22	947	87.8	188	10	US- Sequence 5, Applicatio	4.48e-84
23	945	87.7	207	9	US- Sequence 13, Applicati	7.21e-84
24	945	87.7	207	10	US- Sequence 13, Applicati	7.21e-84
25	945	87.7	207	10	US- Sequence 13, Applicati	7.21e-84
26	945	87.7	207	9	US- Sequence 13, Applicati	7.21e-84
27	945	87.7	207	9	US- Sequence 13, Applicati	7.21e-84
28	899	83.4	221	14	US- Sequence 2, Applicatio	4.06e-79
29	899	83.4	221	8	US- Sequence 2, Applicatio	4.06e-79
30	899	83.4	221	8	US- Sequence 2, Applicatio	4.06e-79
31	897	83.2	133	10	US- Sequence 9, Applicatio	6.54e-79
32	897	83.2	133	10	US- Sequence 9, Applicatio	6.54e-79
33	897	83.2	133	9	US- Sequence 9, Applicatio	6.54e-79
34	897	83.2	133	8	US- Sequence 9, Applicatio	6.54e-79
35	897	83.2	133	9	US- Sequence 9, Applicatio	6.54e-79
36	897	83.2	133	10	US- Sequence 9, Applicatio	6.54e-79
37	897	83.2	133	9	US- Sequence 9, Applicatio	6.54e-79
38	891	82.7	221	12	US- Sequence 5, Applicatio	2.72e-78
39	870	80.7	195	9	US- Sequence 7, Applicatio	3.99e-76
40	870	80.7	195	9	US- Sequence 7, Applicatio	3.99e-76
41	870	80.7	195	10	US- Sequence 7, Applicatio	3.99e-76
42	870	80.7	195	10	US- Sequence 7, Applicatio	3.99e-76
43	870	80.7	195	9	US- Sequence 7, Applicatio	3.99e-76
44	870	80.7	195	8	US- Sequence 7, Applicatio	3.99e-76
45	870	80.7	195	8	US- Sequence 7, Applicatio	3.99e-76

ALIGNMENTS

RESULT	ID	US-08-569-063A-11	STANDARD:	PRT:	188 AA.
XX	AC	xxxxxx			
DE	XX	Sequence 11, Application US/08569063A			
CC	CC	Sequence 11, Application US/08569063A			
CC	CC	GENERAL INFORMATION:			
CC	CC	APPLICANT: ERIKSSON, Ulf			
CC	CC	APPLICANT: OLOFSSON, Birgitta			
CC	CC	APPLICANT: ALITALO, Kari			
CC	CC	APPLICANT: PATUSOLA, Katri			
CC	CC	TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND			
CC	CC	NUMBER OF SEQUENCES: 15			
CC	CC	TITLE OF INVENTION: DNA CODING THEREFOR			
CC	CC	ADDRESS: Evenson, McKeown, Edwards & Lenahan			
CC	CC	STREET: 1200 G Street, N.W., Suite 700			
CC	CC	CITY: Washington			
CC	CC	STATE: DC			
CC	CC	ZIP: 20005			
CC	CC	COMPUTER READABLE FORM:			
CC	CC	MEDIUM TYPE: Floppy disk			
CC	CC	COMPUTER: IBM PC compatible			
CC	CC	OPERATING SYSTEM: PC-DOS/MS-DOS			
CC	CC	SOFTWARE: PatentIn Release #1.0, Version #1.25			
CC	CC	CURRENT APPLICATION DATA:			
CC	CC	APPLICATION NUMBER: US/08/569,063A			
CC	CC	FILING DATE:			
CC	CC	CLASSIFICATION: 435			
CC	CC	PRIOR APPLICATION DATA:			
CC	CC	APPLICATION NUMBER: US 08/469,427			
CC	CC	FILING DATE: 06-JUN-1995			
CC	CC	APPLICATION NUMBER: US 08/397,651			
CC	CC	FILING DATE: 01-MAR-1995			
CC	CC	ATTORNEY/AGENT INFORMATION:			
CC	CC	NAME: EVANS, Joseph D.			
CC	CC	REGISTRATION NUMBER: 26,269			
CC	CC	REFERENCE/DOCKET NUMBER: 41979CP2			
CC	CC	TELECOMMUNICATION INFORMATION:			
CC	CC	TELEPHONE: (202) 628-8800			
CC	CC	TELEFAX: (202) 628-8844			

MORSE

(TM)

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MSrch_PP protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Sep 18 13:52:52 1998; Maspar time 2.12 Seconds
Tabular output not generated. 475.687 Million cell updates/sec

Title: >US-08-765-588-8
Description: (1-143) from US08765588.dep
Perfect Score: 1078
Sequence: 1 MSPILRLTLALLIQLAPAQ.....CRPKKDSAVKPDRCRLRR 143

Scoring table:
PAM 150
Gap 11

Searched: 77021 seqs, 7058996 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5_COMB 2:PCT9_COMB 3:backfiles1

Statistics: Mean 28.064; Variance 116.805; scale 0.240

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1023	94.9	188	1	US-08-469- Sequence 11, Applicat	1.69e-91
2	947	87.8	188	1	US-08-469- Sequence 5, Applicat	1.26e-84
3	897	83.2	133	1	US-08-469- Sequence 9, Applicat	1.12e-78
4	870	80.7	193	1	US-08-469- Sequence 7, Applicat	6.18e-76
5	709	65.8	102	1	US-08-469- Sequence 2, Applicat	1.21e-59
6	400	37.1	121	3	5219739-20 Patent No. 5219739	8.12e-29
7	400	37.1	121	3	5194596-19 Patent No. 5194596	8.12e-29
8	379	35.2	231	2	PCT-US96-0 Sequence 10, Applicat	9.28e-27
9	378	35.1	191	3	5332671-4 Patent No. 5332671	1.16e-26
10	377	33.0	165	3	5219739-19 Patent No. 5219739	1.46e-26
11	377	33.0	165	3	5194596-18 Patent No. 5194596	1.46e-26
12	375	34.8	120	3	5219739-9 Patent No. 5219739	2.28e-26
13	375	34.8	120	3	5194596-9 Patent No. 5194596	2.28e-26
14	374	34.7	215	3	5219739-22 Patent No. 5219739	2.86e-26
15	373	34.6	215	3	5240848-11 Patent No. 5240848	3.58e-26
16	373	34.6	215	3	5240848-7 Patent No. 5240848	3.58e-26
17	365	33.9	190	3	5332671-3 Patent No. 5332671	4.01e-24
18	352	32.7	164	3	5219739-18 Patent No. 5219739	4.01e-24
19	352	32.7	164	3	5219739-17 Patent No. 5219739	4.01e-24
20	352	32.7	164	3	5194596-17 Patent No. 5194596	4.01e-24
21	348	32.3	189	1	US-08-469- Sequence 15, Applicat	9.82e-24
22	318	29.5	149	1	US-08-469- Sequence 14, Applicat	7.59e-21
23	175	16.2	419	2	PCT-US96-0 Sequence 2, Applicat	2.29e-07

24	172	16.0	109	1	US-08-094- Sequence 3, Applicat	4.28e-07
25	172	16.0 <th>109</th> <th>1</th> <th>US-08-094- Sequence 5, Applicat</th> <th>4.28e-07</th>	109	1	US-08-094- Sequence 5, Applicat	4.28e-07
26	170	15.8 <th>109</th> <th>3</th> <th>5498600-3 Patent No. 5498600</th> <th>6.49e-07</th>	109	3	5498600-3 Patent No. 5498600	6.49e-07
27	170	15.8 <th>109</th> <th>1</th> <th>US-08-094- Sequence 4, Applicat</th> <th>6.49e-07</th>	109	1	US-08-094- Sequence 4, Applicat	6.49e-07
28	170	15.8 <th>109</th> <th>1</th> <th>US-08-094- Sequence 2, Applicat</th> <th>6.49e-07</th>	109	1	US-08-094- Sequence 2, Applicat	6.49e-07
29	170	15.8 <th>109</th> <th>1</th> <th>PCT-US93-0 Sequence 1, Applicat</th> <th>6.49e-07</th>	109	1	PCT-US93-0 Sequence 1, Applicat	6.49e-07
30	170	15.8 <th>109</th> <th>2</th> <th>PCT-US91-0 Sequence 16, Applicat</th> <th>6.49e-07</th>	109	2	PCT-US91-0 Sequence 16, Applicat	6.49e-07
31	170	15.8 <th>120</th> <th>3</th> <th>5428135-2 Patent No. 5428135</th> <th>6.49e-07</th>	120	3	5428135-2 Patent No. 5428135	6.49e-07
32	170	15.8 <th>220</th> <th>1</th> <th>5175255-4 Patent No. 5175255</th> <th>6.49e-07</th>	220	1	5175255-4 Patent No. 5175255	6.49e-07
33	170	15.8 <th>226</th> <th>3</th> <th>5498600-2 Patent No. 5498600</th> <th>6.49e-07</th>	226	3	5498600-2 Patent No. 5498600	6.49e-07
34	170	15.8 <th>226</th> <th>3</th> <th>5194596-15 Patent No. 5194596</th> <th>6.49e-07</th>	226	3	5194596-15 Patent No. 5194596	6.49e-07
35	170	15.8 <th>241</th> <th>3</th> <th>5175255-2 Patent No. 5175255</th> <th>6.49e-07</th>	241	3	5175255-2 Patent No. 5175255	6.49e-07
36	170	15.8 <th>241</th> <th>3</th> <th>5175255-8 Patent No. 5175255</th> <th>6.49e-07</th>	241	3	5175255-8 Patent No. 5175255	6.49e-07
37	170	15.8 <th>241</th> <th>3</th> <th>5219739-15 Patent No. 5219739</th> <th>6.49e-07</th>	241	3	5219739-15 Patent No. 5219739	6.49e-07
38	170	15.8 <th>241</th> <th>2</th> <th>PCT-US96-0 Sequence 9, Applicat</th> <th>6.49e-07</th>	241	2	PCT-US96-0 Sequence 9, Applicat	6.49e-07
39	170	15.8 <th>241</th> <th>1</th> <th>US-08-387- Sequence 4, Applicat</th> <th>6.49e-07</th>	241	1	US-08-387- Sequence 4, Applicat	6.49e-07
40	170	15.8 <th>282</th> <th>1</th> <th>US-08-445- Sequence 1, Applicat</th> <th>6.49e-07</th>	282	1	US-08-445- Sequence 1, Applicat	6.49e-07
41	170	15.6 <th>241</th> <th>1</th> <th>US-08-469- Sequence 13, Applicat</th> <th>1.83e-06</th>	241	1	US-08-469- Sequence 13, Applicat	1.83e-06
42	168	15.3 <th>196</th> <th>1</th> <th>US-08-469- Sequence 4, Applicat</th> <th>2.24e-06</th>	196	1	US-08-469- Sequence 4, Applicat	2.24e-06
43	164	15.2 <th>125</th> <th>2</th> <th>PCT-US92-0 Sequence 8, Applicat</th> <th>2.24e-06</th>	125	2	PCT-US92-0 Sequence 8, Applicat	2.24e-06
44	164	15.2 <th>196</th> <th>2</th> <th>PCT-US96-0</th> <th></th>	196	2	PCT-US96-0	

ALIGNMENTS

RESULT	1	STANDARD:	PRT:	188 AA.
XX	US-08-469-427A-11			
AC	xxxxxx			
XX				
DE	Sequence 11, Application US/08469427A			
CC	Sequence 11, Application US/08469427A			
CC	Patent No. 5607918			
CC	GENERAL INFORMATION:			
CC	APPLICANT: Eriksson, Ulf			
CC	APPLICANT: Olafsson, Birgitta			
CC	APPLICANT: Alitalo, Kari			
CC	APPLICANT: Pajusola, Katri			
CC	TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND			
CC	TITLE OF INVENTION: DNA CODING THEREFOR			
CC	NUMBER OF SEQUENCES: 17			
CC	CORRESPONDENCE ADDRESS:			
CC	ADDRESSEE: Evenson, McKewen, Edwards & Lenahan			
CC	STREET: 1200 G Street, N.W., Suite 700			
CC	CITY: Washington			
CC	STATE: DC			
CC	ZIP: 20005			
CC	COMPUTER READABLE FORM:			
CC	MEDIUM TYPE: Floppy disk			
CC	COMPUTER: IBM PC compatible			
CC	OPERATING SYSTEM: PC-DOS/MS-DOS			
CC	SOFTWARE: Patent Release #1.0, Version #1.25			
CC	CURRENT APPLICATION DATA:			
CC	APPLICATION NUMBER: US/08/469,427A			
CC	CLASSIFICATION: 435			
CC	FILING DATE: 06-JUN-1995			
CC	PRIOR APPLICATION DATA:			
CC	APPLICATION NUMBER: US 08/397,651			
CC	FILING DATE: 01-MAR-1995			
CC	ATTORNEY/AGENT INFORMATION:			
CC	NAME: Evans, Joseph D			
CC	REGISTRATION NUMBER: 26,269			
CC	REFERENCE/DOCKET NUMBER: 419799P2			
CC	TELECOMMUNICATION INFORMATION:			
CC	TELEPHONE: (202) 628-8800			
CC	TELEFAX: (202) 628-8844			
CC	INFORMATION FOR SEQ ID NO: 11:			
CC	SEQUENCE CHARACTERISTICS:			
CC	LENGTH: 188 amino acids			

W00727

(TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:47:38 1998; Maspar time 5.75 Seconds

Tabular output not generated. 402.740 Million cell updates/sec

Title: >US-08-765-588-8

Description: (1-143) from US08765588.pep

Perfect Score: 1078

Sequence: 1 MSPLRLRLALALQLAPAO.....CRPKKDSAVKPCRCRLRR 143

Scoring table: PAM 150

Gap 11

Searched: 131922 segs, 16180660 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

a-geneseq32

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 30.138; Variance 121.083; scale 0.249

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	1078	100.0	143	19	W00727	Vascular endothelial	1.31e-99
2	1023	94.9	188	19	W00726	Vascular endothelial	8.25e-94
3	1023	94.9	188	21	W04829	Fibrosarcoma vascular	8.25e-94
4	1023	94.9	207	21	W04831	Vascular endothelial	8.25e-94
5	1023	94.9	207	19	W00725	Vascular endothelial	8.25e-94
6	947	87.8	188	21	W04836	Heart vascular endoth	8.22e-86
7	947	87.8	207	21	W04830	Vascular endothelial	8.22e-86
8	937	86.9	188	19	W00864	Murine VEGF167.	9.25e-85
9	937	86.9	207	19	W00863	Murine VEGF186.	9.25e-85
10	899	83.4	221	23	W07611	Human vascular endoth	9.06e-81
11	897	83.2	133	21	W04828	Vascular endothelial	1.47e-80
12	870	80.7	195	21	W04827	Heart vascular endoth	1.00e-77
13	749	69.5	101	19	W00728	Vascular endothelial	4.56e-65
14	709	65.8	102	21	W04824	Vascular endothelial	6.74e-61
15	411	38.1	377	18	W00586	SAP-AlaMet-VEGF121.	3.27e-30
16	411	38.1	500	18	W00589	SAP-AlaMet-VEGF121-G1	3.27e-30
17	411	38.1	506	18	W00588	SAP-AlaMet-VEGF121/G1	3.27e-30
18	411	38.1	512	18	W00590	SAP-AlaMet-VEGF121/G1	3.27e-30

19	405	37.6	146	5	R27354	Sequence of vascular
20	405	37.6 <th>146</th> <th>4</th> <th>R23348</th> <th>Alternative form of V</th>	146	4	R23348	Alternative form of V
21	404	37.5	148	18	R94032	VEGF121 Cys+2.
22	404	37.5	384	18	R94071	SAP(Gly4Ser)VEGF121.
23	404	37.5	399	18	W00587	SAP(Gly4Ser)4VEGF121.
24	404	37.5	514	18	R94073	SAP(Gly4Ser)VEGF121/G
25	404	37.5	524	18	W00594	SAP(Gly4Ser)2VEGF121(
26	401	37.2	147	18	R94001	VEGF121.
27	401	37.2	147	16	R91075	Human vascular endoth
28	400 <th>37.1</th> <th>121</th> <th>7</th> <th>R42607</th> <th>Human VEGF-121.</th>	37.1	121	7	R42607	Human VEGF-121.
29	400 <th>37.1</th> <th>121</th> <th>3</th> <th>R11385</th> <th>Human vascular endoth</th>	37.1	121	3	R11385	Human vascular endoth
30	395 <th>36.6</th> <th>148</th> <th>18</th> <th>R94031</th> <th>VEGF121 Cys+4.</th>	36.6	148	18	R94031	VEGF121 Cys+4.
31	390 <th>36.2</th> <th>195</th> <th>18</th> <th>W00595</th> <th>SAP-GlySer-VEGF165(G1</th>	36.2	195	18	W00595	SAP-GlySer-VEGF165(G1
32	388 <th>36.0</th> <th>421</th> <th>18</th> <th>W00584</th> <th>SAP-AlaMet-VEGF165.</th>	36.0	421	18	W00584	SAP-AlaMet-VEGF165.
33	388 <th>36.0</th> <th>588</th> <th>18</th> <th>W00592</th> <th>SAP-AlaMet-VEGF165-G1</th>	36.0	588	18	W00592	SAP-AlaMet-VEGF165-G1
34	388 <th>36.0</th> <th>594</th> <th>18</th> <th>W00591</th> <th>SAP(Gly4Ser)VEGF165(G</th>	36.0	594	18	W00591	SAP(Gly4Ser)VEGF165(G
35	388 <th>36.0</th> <th>600</th> <th>18</th> <th>W00593</th> <th>SAP-AlaMet-VEGF165(G1</th>	36.0	600	18	W00593	SAP-AlaMet-VEGF165(G1
36	381 <th>35.3</th> <th>192</th> <th>18</th> <th>R94040</th> <th>VEGF165 Cys+2.</th>	35.3	192	18	R94040	VEGF165 Cys+2.
37	381 <th>35.3</th> <th>428</th> <th>18</th> <th>R94072</th> <th>SAP(Gly4Ser)VEGF165.</th>	35.3	428	18	R94072	SAP(Gly4Ser)VEGF165.
38	381 <th>35.3</th> <th>443</th> <th>18</th> <th>W00585</th> <th>SAP(Gly4Ser)4VEGF165.</th>	35.3	443	18	W00585	SAP(Gly4Ser)4VEGF165.
39	381 <th>35.3</th> <th>598</th> <th>18</th> <th>R94074</th> <th>SAP(Gly4Ser)VEGF165(G</th>	35.3	598	18	R94074	SAP(Gly4Ser)VEGF165(G
40	381 <th>35.3</th> <th>612</th> <th>18</th> <th>W00596</th> <th>SAP(Gly4Ser)2VEGF165(</th>	35.3	612	18	W00596	SAP(Gly4Ser)2VEGF165(
41	378 <th>35.1</th> <th>191</th> <th>27</th> <th>W38242</th> <th>Vascular endothelial</th>	35.1	191	27	W38242	Vascular endothelial
42	378 <th>35.1</th> <th>191</th> <th>18</th> <th>R94002</th> <th>VEGF165.</th>	35.1	191	18	R94002	VEGF165.
43	378 <th>35.1</th> <th>191</th> <th>16</th> <th>R08002</th> <th>Human vascular endoth</th>	35.1	191	16	R08002	Human vascular endoth
44	378 <th>35.1</th> <th>191</th> <th>16</th> <th>R91076</th> <th>Human vascular endoth</th>	35.1	191	16	R91076	Human vascular endoth
45	378 <th>35.1</th> <th>592</th> <th>27</th> <th>W38233</th> <th>VEGF/CPG2 fusion prot</th>	35.1	592	27	W38233	VEGF/CPG2 fusion prot

ALIGNMENTS

RESULT 1
ID W00727 standard; Protein; 143 AA.
AC W00727;
DE 30-NOV-1996 (first entry)
DE Vascular endothelial growth factor-like protein SOM175-e6+e7.
KW Vascular endothelial growth factor; VEGF; SOM175-e6+e7; neuron;
OS Homo sapiens.
FH Key Location/Qualifiers
FT peptide 1..21
FT /label= Sig_peptide
PI W0627007-A1.
PD 06-SEP-1996.
PE 22-FEB-1996; AUT0094.
PR 02-MAR-1995; AU-001457.
PR 20-NOV-1995; AU-006647.
PR 22-DEC-1995; AU-007274.
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
PI Grimmond S, Hayward NK, Larsson C, Nordenskjold M;
PI Weber G;
DR WPI: 96-412774/41.
DR N-PSDB; T33612.
PT New growth factor related to vascular endothelial growth factor
PT useful for inducing astroglial proliferation and promoting neuronal
PT survival
PS Claim 13; Page 46; 113pp; English.
CC Spline variants (W00726-28) of the human vascular endothelial growth
CC factor-like polypeptide SOM175 (see also W00725) are products of
CC cDNA clones (see also T33611-13) respectively lacking exon 6, exons
CC 6-7, and exon 4 of the SOM175 gene (see also T33610). They show at
CC least 1 of the properties of SOM175 including the ability to induce
CC proliferation of vascular endothelial cells, to interact with
CC fit-1/fik-1 receptors, and to induce cell migration, cell survival
CC and/or an increase in intracellular levels of alkaline phosphatase.
CC Recombinant SOM175 proteins can be used to induce astroglial
CC proliferation and to promote neural survival and/or proliferation.
SQ Sequence 143 AA;
Query Match 100.0%; Score 1078; DB 19; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.31e-99;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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MSPRCH_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:42:57 1998; Maspar time 10.92 Seconds

Tabular output not generated. 724.739 Million cell updates/sec

Title: >US-08-765-588-6
Description: (1-188) from US08765588.pep
Perfect Score: 1458
Sequence: 1 MSPRLRLALLALQAPAPQ.....COGRGLENPDCRCRKLRR 188

Scoring table: PAM 150
Gap 11

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

sptrembl6
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phase 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 41.227; Variance 70.997; scale 0.581

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1014	69.5	207	2	VEGF RELATED FACTOR IS	4.54e-210
2	938	64.3	207	10	VASCULAR ENDOTHELIAL G	1.12e-191
3	611	41.9	116	10	VASCULAR ENDOTHELIAL G	1.80e-113
4	497	34.1	194	12	VASCULAR ENDOTHELIAL G	9.00e-87
5	371	25.4	232	2	VASCULAR ENDOTHELIAL G	6.76e-58
6	365	25.0	148	12	VASCULAR ENDOTHELIAL G	1.52e-56
7	330	22.6	216	12	VASCULAR ENDOTHELIAL G	1.02e-48
8	278	19.1	75	4	VASCULAR ENDOTHELIAL G	2.67e-37
9	268	18.4	158	10	PLACENTA GROWTH FACTOR	3.85e-35
10	198	13.6	358	10	VASCULAR ENDOTHELIAL G	1.78e-20
11	192	13.2	326	10	VASCULAR ENDOTHELIAL G	2.88e-19
12	188	12.9	415	10	VASCULAR ENDOTHELIAL G	1.82e-18
13	177	12.1	271	11	POLYPEPTIDE PRECURSOR	2.76e-16
14	170	11.7	185	2	C-SIS PRMO-ONCOGENE (6.45e-15
15	168	11.5	210	4	C-SIS ONCOGENE (PLATL	1.58e-14
16	147	10.1	183	10	PDGF PROTEIN (FRAGMENT	1.52e-10
17	128	8.8	126	10	VASCULAR ENDOTHELIAL G	4.15e-07
18	101	6.9	324	10	FAS ANTIGEN PRECURSOR	1.31e-02
19	99	6.8	749	3	SPID PRECURSOR (FRAGME	2.69e-02
20	97	6.7	952	9	GLYCINE DEHYDROGENASE	5.44e-02

21	95	6.5	292	9	P74446	HYPOTHETICAL 32.3 KD P	1.09e-01
22	94	6.4	180	3	Q99072	GIANT SECRETORY PROTEI	1.54e-01
23	94	6.4	187	3	Q23782	BRC GENE (3'END) IN BA	1.54e-01
24	93	6.4	391	3	Q26258	BR2-2-BALBANT RING (5	2.17e-01
25	93	6.4	411	8	Q38946	GLUTAMATE DEHYDROGENAS	3.05e-01
26	92	6.3	68	11	Q84667	GENOME PARTIAL SEQUEN	4.27e-01
27	91	6.2	139	3	Q00830	(FRAGMENT)	4.27e-01
28	91	6.2	235	3	Q94441	REPEITIVE DNA IN BALB	4.27e-01
29	90	6.2	240	3	Q23780	BRC GENE PRODUCT (FRAG	5.98e-01
30	89	6.1	571	9	Q51763	IS1162 DNA	8.33e-01
31	87	6.0	112	8	Q40726	DNA BINDING PROTEIN (F	1.61e+00
32	87	6.0	411	8	Q04937	NAOH GLUTAMATE DEHIDRO	1.61e+00
33	88	6.0	1260	2	Q15047	KIRA00339.	1.16e+00
34	87	6.0	2796	9	Q48926	FATTY ACID SYNTHASE.	1.61e+00
35	86	5.9	105	9	Q60232	INCE PLASMID REPRIB RE	2.22e+00
36	86	5.9	394	9	Q96447	EXR46.	2.22e+00
37	86	5.9	470	3	Q22919	COSMID C37C3.	2.22e+00
38	86	5.9	605	2	Q00304	VOLTAGE-DEPENDENT CALC	2.22e+00
39	86	5.9	722	11	Q89466	TEGUMENT PROTEIN.	2.22e+00
40	86	5.9	919	4	Q28659	FERTILIN ALPHA SUBUNIT	2.22e+00
41	86	5.8	1704	3	Q94446	220 KDA SILK PROTEIN.	2.22e+00
42	85	5.8	411	8	Q43260	GLUTAMATE DEHYDROGENAS	3.06e+00
43	85	5.8	411	8	Q04872	GLUTAMATE DEHYDROGENAS	3.06e+00
44	85	5.8	412	8	Q93541	GLUTAMATE DEHYDROGENAS	3.06e+00
45	85	5.8	1269	2	Q13045	FLIT (HOMOLOG OF D. ME	3.06e+00

ALIGNMENTS

RESULT ID	1	PRELIMINARY	PRT	207 AA.
AC	Q16528:			
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)			
DE	VEGF RELATED FACTOR ISOFORM VRF186 PRECURSOR.			
GS	VRE OR VEGF-B.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; NEUKOTA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUETHERIA; PRIMATES.			
OC	[1]			
RP	SEQUENCE FROM N.A.			
RC	GRIMMOND S., LAGERGRANTZ J., DRINKWATER C., SILINS G., TOMNISON S.,			
RA	POLLACK P., GOTLEY D., CARSON E., RAKAR S., NORDENSKOLD M., WARD L.,			
RA	HAYWARD N., WEBER G.,			
RL	GENOME RES. 6:122-129(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-FIBROSARCOMA HT-1080;			
RC	MEDLINE; 96197355.			
RA	OLOFFSON B.,			
RL	PROC. NATL. ACAD. SCI. U.S.A. 93:2576-2581(1996).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-FIBROSARCOMA HT-1080;			
RC	MEDLINE; 96325041.			
RA	OLOFFSON B., PAJUSOLA K., VON EULER G., CHILOV D., ALITALO K.,			
RA	ERIKSSON U.,			
RL	J. BIOL. CHEM. 271:19310-19317(1996).			
DR	EMBL; U43368; G12163366; .			
DR	EMBL; U52818; G1488259; .			
DR	PROSITE; PS00249; PDGF; 1.			
KW	SIGNAL.			
FT	SIGNAL.			
FT	CHAIN			
SO	SEQUENCE			
Query Match	69.5%;	Score 1014;	DB 2;	Length 207;
Best Local Similarity	100.0%;	Pred. No. 4.54e-210;		
Matches	136;	Conservative	0;	Mismatches 0;
			Indels 0;	Gaps 0;
Db	1 MSPRLRLALLALQAPAPVSGPAPGHQRKRVSMIDVYTRANQPREVVVPLTVEL 60			

 W O R L D

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MPSEARCH protein - protein database search, using Smith-Waterman algorithm
 Run on: Fri Sep 18 13:41:41 1998; Maspar time 6.16 Seconds
 Tabular output not generated. 765.523 Million cell updates/sec

Title: >US-08-765-588-6
 Description: (1-188) from US08765588.pep
 Perfect Score: 1458
 Sequence: 1 MSPFLRLTLAALLQAPAQ.....CQGRGLNPDTCCRCRLR 188

Scoring table:
 Gap 11
 Gap 11

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot35
 1:swiss1

Statistics: Mean 43.185; Variance 67.718; scale 0.638

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.	
1	1458	100.0	188	1	VEGF_HUMAN	VASCULAR ENDOTHELIAL G	0.00e+00
2	1317	90.3	188	1	VEGF_MOUSE	VASCULAR ENDOTHELIAL G	0.00e+00
3	513	35.2	190	1	VEGF_RAT	VASCULAR ENDOTHELIAL G	1.45e-98
4	511	35.0	190	1	VEGF_PIG	VASCULAR ENDOTHELIAL G	4.68e-98
5	505	34.6	190	1	VEGF_BOVIN	VASCULAR ENDOTHELIAL G	1.57e-96
6	498	34.2	164	1	VEGF_CAVPO	VASCULAR ENDOTHELIAL G	9.43e-95
7	371	25.4	215	1	VEGF_HUMAN	VASCULAR ENDOTHELIAL G	5.87e-63
8	369	25.3	214	1	VEGF_SHEEP	VASCULAR ENDOTHELIAL G	1.82e-62
9	369	25.3	214	1	VEGF_MOUSE	VASCULAR ENDOTHELIAL G	9.05e-61
10	321	22.0	170	1	PLGF_HUMAN	PLACENTA GROWTH FACTOR	8.94e-45
11	296	20.3	133	1	VEGF_ORF2	VASCULAR ENDOTHELIAL G	8.41e-45
12	275	18.9	158	1	PLGF_MOUSE	PLACENTA GROWTH FACTOR	1.60e-36
13	281	17.9	128	1	VEGF_COTUA	VASCULAR ENDOTHELIAL G	1.51e-18
14	181	12.4	225	1	PDGF_RAT	VASCULAR ENDOTHELIAL G	6.60e-18
15	178	12.2	419	1	VEGF_HUMAN	VASCULAR ENDOTHELIAL G	1.08e-17
16	177	12.1	226	1	TSIS_SMSAV	PDGF-RELATED TRANSFORM	1.08e-17
17	177	12.1	241	1	PDGF_MOUSE	PLATELET-DERIVED GROWT	1.08e-17
18	177	12.1	241	1	PDGF_HUMAN	PLATELET-DERIVED GROWT	1.08e-17
19	176	12.1	245	1	PDGF_FELCA	PLATELET-DERIVED GROWT	1.76e-17
20	174	11.9	148	1	VEGF_ORF7	VASCULAR ENDOTHELIAL G	4.66e-17
21	171	11.7	213	1	PDGF_RABIT	PLATELET-DERIVED GROWT	2.00e-16
22	169	11.6	211	1	PDGF_HUMAN	PLATELET-DERIVED GROWT	5.26e-16
23	165	11.3	211	1	PDGF_MOUSE	PLATELET-DERIVED GROWT	3.60e-15

RESULT ID	VEGF_HUMAN	STANDARD	PRT	188 AA	ALIGNMENTS
AC	P49765				
DT	01-OCT-1996 (REL. 34, CREATED)				
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)				
DE	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR).				
GN	VEGF OR VRF.				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;				
OC	EUTHERIA; PRIMATES.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 9619735.				
RA	OLOFSSON B., PAUSOLA K., KAIPAINEN A., VON EULER G., JOIKOV V.,				
RA	SAXSELA O., ORPANA A., PETTERSSON R.F., ALTALO K., ERIKSSON U.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 93:2576-2581(1996).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	GRIMMOND S., LAGERCRANTZ J., DRINKWATER C., SILINS G., TOWNSON S.,				
RA	POLLOCK P., GOTLEY D., CARSON E., RAKAR S., NORDENSKOLD M.,				
RA	WARD L., HAYWARD N., WEBER G.;				
RL	GENOME RES. 6:122-129(1996).				
CC	- FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BINDS HEPARIN.				
CC	- SUBUNIT: HOMODIMER, DISULFIDE-LINKED. CAN ALSO FORM HETERODIMER WITH VEGF.				
CC	- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN.				
CC	- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXCEPT LIVER.				
CC	HIGHEST LEVELS FOUND IN HEART, SKELETAL MUSCLE AND PANCREAS.				
CC	- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.				
DR	EMBL; U48801; G1234823; -				
DR	EMBL; U43369; G1216398; -				
DR	MIM; 601398; -				
KW	PROSITE; PS00249; PDGF; 1.				
KW	MITOGEN; GROWTH FACTOR; SIGNAL; HEPARIN-BINDING.				
FT	SIGNAL				
FT	CHAIN				
SO	SEQUENCE				

Query Match 100.0%; Score 1458; DB 1; Length 188;
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 MSPFLRLTLAALLQAPAQVSPDAPGHQRVSVSDVYTRATQCPREVVYPLVTEL 60

MORSE

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Msrch.p protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:40:03 1998; Maspar time 9.36 Seconds

Tabular output not generated. 734.106 Million cell updates/sec

Title: >US-08-765-588-6
Description: (1-188) from US08765588.pep
Perfect Score: 1458
Sequence: 1 MSPILRLRLALALQAPAO.....COGRGLENDPCRCRKLRR 188

Scoring table: PAM 150
Gap 11

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

plrs6
1:plrl 2:plrl 3:plrl 4:plrl 5:nlrl3d

Statistics: Mean 41.161; Variance 80.141; scale 0.514

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1317	90.3	188	2	JC4680	5.71e-251
2	938	64.3	207	2	JC4679	2.15e-169
3	513	35.2	190	2	A35987	7.43e-80
4	511	35.0	190	2	S52130	1.92e-79
5	509	34.9	190	2	B44881	4.95e-79
6	505	34.6	190	2	B40080	3.30e-78
7	371	25.4	232	2	A41551	5.30e-51
8	369	25.3	146	2	S57956	1.33e-50
9	369	25.3	214	2	A44881	1.33e-50
10	361	24.8	120	2	A33787	5.22e-49
11	296	20.3	143	2	A41236	1.33e-36
12	295	20.2	133	2	B49530	4.84e-36
13	268	18.4	158	2	A56125	7.49e-31
14	261	17.9	128	2	S51295	1.61e-29
15	181	12.4	225	2	S25097	7.66e-15
16	178	12.2	419	2	S69207	2.56e-14
17	177	12.1	161	2	138108	3.83e-14
18	177	12.1	226	1	TYWVSS	3.83e-14
19	177	12.1	230	2	AVW030	3.83e-14
20	177	12.1	241	1	PFMSGB	3.83e-14
21	177	12.1	241	1	PFHUG2	3.83e-14
22	176	12.1	245	1	TYVCTSS	5.72e-14
23	174	11.9	148	2	DA9530	1.27e-13

24	171	11.7	166	2	UN0248	platelet-derived grow	4.21e-13
25	170	11.7	185	2	S58383	hypothetical protein	6.26e-13
26	171	11.7	198	2	J50735	platelet-derived grow	4.21e-13
27	169	11.6	211	1	PFHUG1	platelet-derived grow	9.31e-13
28	165	11.3	215	2	S08220	platelet-derived grow	4.52e-12
29	164	11.2	196	2	B28964	platelet-derived grow	6.69e-12
30	164	11.2	197	2	S25096	platelet-derived grow	6.69e-12
31	163	11.2	200	2	I51551	platelet-derived grow	9.91e-12
32	163	11.2	226	2	I51550	platelet-derived grow	9.91e-12
33	163	11.2	271	2	A25669	PGF-related transfor	9.91e-12
34	161	11.0	196	2	A37359	platelet-derived grow	2.17e-11
35	153	10.5	63	5	1PDGB2	platelet-derived grow	4.80e-10
36	153	10.5	66	5	1PDGC2	platelet-derived grow	4.80e-10
37	153	10.5	68	5	1PDGA2	platelet-derived grow	4.80e-10
38	145	9.9	196	2	A48851	platelet-derived grow	1.01e-08
39	107	7.3	3707	2	S18252	heparan sulfate prote	7.58e-03
40	101	6.9	324	2	UC2395	ras antigen - rat	5.33e-02
41	99	6.8	749	2	A45294	Balbiani ring 2.1 - m	1.01e-01
42	99	6.8	4391	2	A58096	perlecan precursor -	1.01e-01
43	96	6.6	100	2	S33338	prolamin p2 - red ho	2.58e-01
44	96	6.6	327	2	A46484	apoptosis-mediating m	2.58e-01
45	95	6.5	292	2	S76418	hypothetical protein	3.51e-01

ALIGNMENTS

ENTRY	1	ALIGNMENTS
TITLE	JC4680	#type complete
ALTERNATE_NAMES	vascular endothelial growth factor-related factor 167 - mouse	
ORGANISM	VRF 167 protein	
DATE	10-May-1996	#sequence_revision 19-Jul-1996 #text_change 10-Sep-1997

ACCESSIONS	REFERENCE
JC4680	Townson, S.; Lagercrantz, J.; Grilmond, S.; Sillins, G.; Nordenskjold, M.; Weber, G.; Hayward, N.
JC4679	Biochem. Biophys. Res. Commun. (1996) 220:922-928

#journal	#title	#accession	#molecule_type	#label	#TOW
1	Journal of Vascular Medicine and Biology	JC4680	mRNA	1-188	91314335

COMMENT: This factor is a mitogen, that is selective for endothelial cells, and belongs to a family of growth factor. This transcript is differentially spliced to produce two major isoforms, vascular endothelial growth factors 167 and VEGF 186.

GENETICS

#gene	#map_position	#introns	#exons
1	13772	19	20

SUMMARY: Query Match 90.3%; Score 1317; DB 2; Length 188; Best local similarity 87.8%; Pred. No. 5.71e-251; Matches 165; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

DB	1	MSPILRLRLALALQAPAOVSPAPAGHQRVSMIDVYATATQCPRRVPLVEL	60
DB	61	MGNVKKDLVSCVTVQRCGCCPDGECVPTGQHYRMQIMQYSSSGESLEHS	120
DB	61	MGTAKOLVSCVTVQRCGCCPDGECVPTGQHYRMQIMQYSSSGESLEHS	120
DB	121	OCBCRPKKESAVKPDSPRLICPCTGRORPDRPCRCRRRRLTCOGGLENDPT	180
DB	121	OCBCRPKKESAVKPDSPRLICPCTGRORPDRPCRCRRRRLTCOGGLENDPT	180

M P E R E L L
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MPsrch.p protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:44:55 1998; Maspar time 2.47 Seconds
537.274 Million cell updates/sec

Tabular output not generated.

Title: >US-08-765-588-6
Description: (1-188) from US08765588.pep
Perfect Score: 1458
Sequence: 1 MSPLRLRLALALQLAPAO.....COGRGLNPDCRCRKLRR 188

Scoring table: PAM 150
Gap 11

Searched: 77021 seqs, 7058996 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5_COMB 2:PCIT9_COMB 3:backfiles1.

Statistics: Mean 29.152; Variance 121.909; scale 0.239

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1458	100.0	188	1	US-08-469- Sequence 11, Applicat	6.66e-135
2	1317	90.3	188	1	US-08-469- Sequence 5, Applicat	1.60e-120
3	1240	85.0	195	1	US-08-469- Sequence 7, Applicat	1.11e-112
4	897	61.5	133	1	US-08-469- Sequence 9, Applicat	6.75e-78
5	709	48.6	102	1	US-08-469- Sequence 2, Applicat	5.58e-59
6	517	35.5	165	3	5194596-18 Patent No. 5194596.	7.46e-40
7	517	35.5	165	3	5219739-19 Patent No. 5219739.	5.94e-40
8	518	35.5	191	3	5332671-4 Patent No. 5332671.	1.15e-38
9	505	34.6	190	3	5332671-3 Patent No. 5332671.	2.20e-37
10	492	33.7	164	3	5219739-18 Patent No. 5219739.	2.20e-37
11	492	33.7	164	3	5194596-17 Patent No. 5194596.	2.20e-37
12	492	33.7	164	3	5219739-17 Patent No. 5219739.	2.20e-37
13	486	33.3	189	1	US-08-469- Sequence 15, Applicat	8.58e-37
14	400	27.4	55	1	US-08-469- Sequence 3, Applicat	2.32e-38
15	383	26.3	121	3	5194596-19 Patent No. 5194596.	1.04e-36
16	383	26.3	121	3	5219739-20 Patent No. 5219739.	1.04e-36
17	377	25.3	231	2	PCT-US96-0 Patent No. 5219739.	1.22e-25
18	372	25.5	214	3	5240848-11 Patent No. 5240848.	1.22e-25
19	372	25.5	215	3	5219739-22 Patent No. 5219739.	1.53e-25
20	371	25.4	215	3	5240848-7 Patent No. 5240848.	1.42e-24
21	361	24.8	120	3	5219739-9 Patent No. 5194596.	1.42e-24
22	361	24.8	120	3	5194596-9 Patent No. 5194596.	2.46e-18
23	296	20.3	149	1	US-08-469- Sequence 14, Applicat	2.46e-18

RESULT ID	Sequence	Standard	PRT	188 AA.			
24	178	12.2	419	2	PCT-US96-0	Sequence 2, Applicat	2.27e-07
25	177	12.1	160	1	US-08-094-	Sequence 1, Applicat	2.79e-07
26	177	12.1	220	3	5175255-4	Patent No. 5175255.	2.79e-07
27	177	12.1	226	3	5498600-2	Patent No. 5498600.	2.79e-07
28	177	12.1	241	3	5175255-2	Patent No. 5175255.	2.79e-07
29	177	12.1	241	3	5175255-8	Patent No. 5175255.	2.79e-07
30	177	12.1	241	3	5194596-15	Patent No. 5194596.	2.79e-07
31	177	12.1	241	3	US-08-387-	Sequence 4, Applicat	2.79e-07
32	177	12.1	241	3	5219739-15	Patent No. 5219739.	2.79e-07
33	177	12.1	241	1	US-08-469-	Sequence 13, Applicat	2.79e-07
34	177	12.1	241	1	PCT-US96-0	Sequence 9, Applicat	2.79e-07
35	172	11.8	109	1	US-08-094-	Sequence 7, Applicat	7.81e-07
36	172	11.8	109	1	US-08-094-	Sequence 5, Applicat	7.81e-07
37	170	11.7	109	3	5498600-3	Patent No. 5498600.	1.18e-06
38	170	11.7	109	2	US-08-094-	Sequence 2, Applicat	1.18e-06
39	170	11.7	109	2	PCT-US93-0	Sequence 1, Applicat	1.18e-06
40	170	11.7	109	1	US-08-094-	Sequence 4, Applicat	1.18e-06
41	170	11.7	109	2	PCT-US91-0	Sequence 18, Applicat	1.18e-06
42	170	11.7	120	3	5428135-2	Patent No. 5428135.	1.18e-06
43	170	11.7	282	1	US-08-445-	Sequence 1, Applicat	1.18e-06
44	169	11.6	125	1	US-07-883-	Sequence 7, Applicat	1.45e-06
45	169	11.6	125	1	US-08-095-	Sequence 4, Applicat	1.45e-06

ALIGNMENTS

Sequence 11, Application US/08469427A

Sequence 11, Application US/08469427A

Patent No. 5607918

GENERAL INFORMATION:

APPLICANT: Eriksson, Ulf

APPLICANT: Olofsson, Birgitta

APPLICANT: Alltalo, Kari

APPLICANT: Pajusola, Katri

TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Evenson, McKeown, Edwards & Lenahan

STREET: 1200 G Street, N.W., Suite 700

CITY: Washington

STATE: DC

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/469,427A

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/397,651

FILING DATE: 01-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Evans, Joseph D

REGISTRATION NUMBER: 26,269

REFERENCE/DOCKET NUMBER: 41979cp2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 628-8800

TELEFAX: (202) 628-8844

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 188 amino acids

(TM)

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t generated.

MSPILR

Gap 11

288199 seqs, 31643258 residues

Listing first 45 summaries

a-pending

17:NEWU6 18:NEWU7 19:NEWU8 20:NEWU9

mean 31.271; variance 155.127; scale 0.202

ved by analysis of the total score distribution.

SUMMARIES

4.5.41

45 8

ALIGNMENTS

[illegible]

Sequence 15, Application US/08609443A
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALLTALO, Kari
APPLICANT: PAUSIOJA, Kari
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
TITLE OF INVENTION: DNA CODING THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
City: Washington
STATE: DC
COUNTRY: US
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,443A
FILING DATE: 01-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569,063
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269

MIPSEPH
(TW)

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MSPRCH.PP protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:32:46 1998; Maspar time 11.91 Seconds
732.057 Million cell updates/sec

Tabular output not generated.

Title: >US-08-765-588-4
Description: (1-207) from US08765588.pep
Sequence: 1 MSPRLRLALALQLAPAQ.....PGPAAADAAASVAKGA 207

Scoring table: PAM 150
Gap 11

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

1:sp.fungi 2:sp.human 3:sp.invertebrate 4:sp.mammal
5:sp.mhc 6:sp.organelle 7:sp.phage 8:sp.plant
9:sp.bacteria 10:sp.rodent 11:sp.virus 12:sp.yeast
13:sp.unclassified

Statistics: Mean 42.614; Variance 109.241; scale 0.390

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1452	100.0	207	2	Q16528 VEGF RELATED FACTOR IS	2.09e-211
2	1319	90.8	207	10	064290 VASCULAR ENDOTHELIAL G	1.59e-189
3	780	53.7	116	10	035485 VASCULAR ENDOTHELIAL G	9.13e-102
4	373	25.7	232	2	Q16889 VASCULAR ENDOTHELIAL G	8.56e-38
5	372	25.6	148	12	042571 VASCULAR ENDOTHELIAL G	1.21e-37
6	361	24.9	194	12	042572 VASCULAR ENDOTHELIAL G	5.56e-36
7	333	22.9	216	12	091420 VASCULAR ENDOTHELIAL G	8.83e-32
8	279	19.2	158	10	063434 PLACENTA GROWTH FACTOR	1.04e-24
9	278	19.1	75	4	018843 VASCULAR ENDOTHELIAL G	1.12e-23
10	198	13.6	358	10	P97946 VASCULAR ENDOTHELIAL G	2.14e-12
11	196	13.5	210	4	Q29613 C-SIS ONCOGENE (PLATEL	4.00e-12
12	192	13.2	326	10	035251 VASCULAR ENDOTHELIAL G	1.39e-11
13	180	12.4	271	11	041283 POLYPROTEIN PRECURSOR	5.55e-10
14	179	12.3	185	2	Q15354 C-SIS PROTO-ONCOGENE (7.52e-10
15	176	12.1	415	10	P97953 VASCULAR ENDOTHELIAL G	1.87e-09
16	162	11.2	183	10	063740 PDGF PROTEIN (FRAGMENT	1.24e-07
17	153	10.5	473	8	Q39620 (VSP-3) PRECURSOR.	1.73e-06
18	143	9.8	581	9	Q20517 F47B8.5.	3.04e-05
19	141	9.7	901	9	Q44562 SIADLASE.	5.35e-05
20	139	9.6	442	8	Q39494 75K MRNA.	9.38e-05

RESULT	ID	Score	Query Match	Length	DB ID	Description	Pred. No.
21	137	9.4	2378	3	P91365	CODED FOR BY C. ELEGAN	1.64e-04
22	134	9.2	552	8	Q96343	MYOSINASE-BINDING PRO	3.78e-04
23	132	9.1	438	8	Q39495	ALPHA 2 FRUSULIN.	6.55e-04
24	130	9.0	371	9	Q06555	HYPOTHEICAL 36.4 KD P	1.13e-03
25	130	9.0	416	3	Q17374	T13B5.4 PROTEIN.	1.13e-03
26	130	9.0	611	9	P74375	HYPOTHEICAL 62.9 KD P	1.13e-03
27	131	9.0	1336	10	Q63729	N-METHYL-D-ASPARTATE R	8.62e-04
28	129	8.9	351	8	Q39492	WP6 PRECURSOR.	1.49e-03
29	129	8.9	375	8	P33066	OLOSIN-LIKE PROTEIN.	1.49e-03
30	129	8.9	376	8	Q39353	CELL WALL-PLASMA MEMB	1.49e-03
31	129	8.9	381	3	Q94399	ZK65.2.	1.49e-03
32	129	8.9	507	12	Q13028	ANTIFREZE GLYCOPETID	1.49e-03
33	128	8.8	151	8	Q41192	NABP3.	1.95e-03
34	128	8.8	196	8	Q08195	CYSTEINE-RICH EXTENSIN	1.95e-03
35	128	8.8	439	8	Q42421	CHITINASE PRECURSOR.	1.95e-03
36	128	8.8	1711	9	P96311	ENOGUCANASE A (EC. 3.	1.95e-03
37	127	8.7	145	8	Q40786	ARABINGALACTIN-PROTEI	2.56e-03
38	127	8.7	153	3	Q00879	MEROZOTIE SURFACE PROT	2.56e-03
39	127	8.7	309	11	Q89402	CONTAINS PRO-RICH PX M	2.56e-03
40	127	8.7	464	8	Q41645	EXTENSIN (FRAGMENT).	2.56e-03
41	127	8.7	801	3	Q23635	SIMILAR TO LONG TANDEM	2.56e-03
42	125	8.6	228	8	Q43558	PROLINE RICH PROTEIN P	4.39e-03
43	125	8.6	616	11	Q96716	DNA BINDING PROTEIN.	4.39e-03
44	124	8.5	496	11	Q98457	GENOME. PARTIAL SEQEN	5.74e-03
45	124	8.5	1000	9	Q24820	BETA-GUCANASE.	5.74e-03

ALIGNMENTS

1 PRELIMINARY; PRT; 207 AA.

AC Q16528; (TREMURREL. 01, CREATED)

DT 01-NOV-1996 (TREMURREL. 01, LAST SEQUENCE UPDATE)

DT 01-JAN-1998 (TREMURREL. 05, LAST ANNOTATION UPDATE)

DE VEGF RELATED FACTOR ISOFORM VRF186 PRECURSOR.

GN VRF OR VEGF-B.

OS HOMO SAPIENS (HUMAN).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; PRIMATES.

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN.

RA	GRIMMOND S., LAGERGRANTZ J., DRINKWATER C., SILLINS G., TOWNSON S.,
RA	POLLOCK P., GOTLEY D., CARSON E., RAKAR S., NORDENSKOLD M., WARD L.,
RA	HAYWARD N., WEBER G.,
RL	GENOME RES. 6:122-129(1996).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE-FIBROSARCOMA HT-1080;

RK MEDLINE; 96197355.

RA OLOFSSON B.,

RL PROC. NATL. ACAD. SCI. U.S.A. 93:2576-2581(1996).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE-FIBROSARCOMA HT-1080;

RK MEDLINE; 96325041.

RA OLOFSSON B., PANTUOLA K., VON ETLER G., CHILOV D., ALITALO K.,

RA ERIKSSON U.,

RL J. BIOL. CHEM. 271:19310-19317(1996).

DR EMBL; U43368; G1216396; -

DR PROSITE; P500249; PDGF; 1.

FT SIGNAL.

FT CHAIN

SO SEQUENCE

207 AA; 21602 MM; 16BDF61 GNC32;

Query Match 100.0%; Score 1452; DB 2; Length 207;

Best Local Similarity 100.0%; Pred. No. 2.09e-211;

Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MSPRLRLALALQLAPAPVSPDAPGHQKRVSMIDVYIRACQPREVVPPLVLEL 60

WORLDWIDE
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Msrch_dp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:31:58 1998; MasPar time 6.68 seconds

Tabular output not generated. 777.434 Million cell updates/sec

Title: >US-08-765-588-4
Description: (1-207) from US08765588.pep
Perfect Score: 1452
Sequence: 1 MSPPLRLTLLAALQAPAO.....PGPAAADAAASVAKGA 207

Scoring table: PAM 150
Gap 11

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 44.541; Variance 104.798; scale 0.425

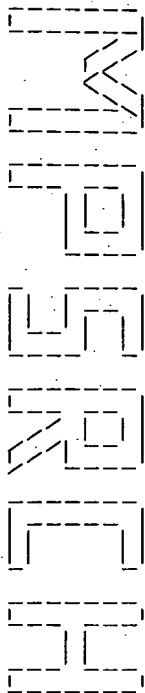
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1014	69.8	188	1	VEGB_HUMAN VASCULAR ENDOTHELIAL G	1.62e-151
2	938	64.6	188	1	VEGB_MOUSE VASCULAR ENDOTHELIAL G	4.30e-138
3	373	25.7	215	1	VEGF_HUMAN VASCULAR ENDOTHELIAL G	5.93e-41
4	371	25.6	190	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	1.26e-40
5	371	25.6	214	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	1.26e-40
6	364	25.1	190	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	1.26e-40
7	361	24.9	146	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	1.26e-40
8	358	24.7	190	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	1.26e-40
9	347	23.9	164	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	1.26e-40
10	306	21.1	170	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	1.26e-40
11	294	20.2	133	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	1.26e-40
12	284	19.6	158	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	1.26e-40
13	264	18.2	128	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	1.26e-40
14	189	13.0	225	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	1.26e-40
15	180	12.4	226	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	1.26e-40
16	180	12.4	241	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	1.26e-40
17	179	12.3	241	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	1.26e-40
18	179	12.3	245	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	1.26e-40
19	175	12.1	419	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	1.26e-40
20	174	12.0	148	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	1.26e-40
21	172	11.8	211	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	1.26e-40
22	172	11.8	213	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	1.26e-40
23	167	11.5	211	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	1.26e-40

ID	VEGB_HUMAN	STANDARD	PRT	188 AA.
AC	P49765;			
DT	01-OCT-1996 (REL. 34, CREATED)			
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)			
DE	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR).			
GN	VEGF-B OR VRE.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUTHERIA; PRIMATES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 96197355.			
RA	OLOFFSON B., PAJUSOLA K., KAIKAINEN A., VON EULER G., JOURKOV V., SAKSELA O., ORPANA A., PETERSSON R.F., ALLITALO K., ERIKSSON U., PROOC. NATL. ACAD. SCI. U.S.A. 93:2576-2581(1996).			
RT	[2]			
RP	SEQUENCE FROM N.A.			
RA	GRIMMOND S., LAGERCRANTZ J., DRINKWATER C., SILINS G., TOWNSON S., POLLOCK P., GOTLEY D., CARSON E., RAKAR S., NORDENSKJOLD M., WARD L., HAYWARD N., WEBER G.;			
RT	GENOME RES. 6:122-129(1996).			
CC	- FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BINDS HEPARIN.			
CC	- SUBUNIT: HOMODIMER, DISULFIDE-LINKED. CAN ALSO FORM HETERODIMER WITH VEGF.			
CC	- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN.			
CC	- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXCEPT LIVER.			
CC	- HIGHEST LEVELS FOUND IN HEART, SKELETAL MUSCLE AND PANCREAS.			
CC	- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.			
DR	EMBL; U48801; G1234823; -			
DR	EMBL; U43369; G1216398; -			
DR	MTM; 601398; -			
DR	PROSITE; PS00249; PDGF; 1.			
KM	MITOGEN; GROWTH FACTOR; SIGNAL; HEPARIN-BINDING.			
FT	SIGNAL			
FT	CHAIN			
SO	SEQUENCE			

Query Match 69.88; Score 1014; DB 1; Length 188;
Best Local Similarity 100.08; Pred. No. 1.62e-151;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MSPPLRLTLLAALQAPAOVSPDAPGHOKYVSMIDVYRANCPREVVPLTVEL 60
|||||



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MPsrch_PP protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Sep 18 13:30:29 1998; MasPar time 9.90 Seconds
Tabular output not generated. 763.780 Million cell updates/sec

Title: >US-08-765-588-4
Description: (1-207) from US08765588.pap
Perfect Score: 1452
Sequence: 1 MSPILRLILALLOLAPAO.....PGRAAAADAAASVAKGA 207

Scoring table: PAM 150
Gap 11

Searched: 120441 seqs, 36531193 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plr56
1:plrl 2:plr2 3:plr3 4:plr4 5:nrl3d

Statistics: Mean 42.396; Variance 117.569; scale 0.361

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1319	90.8	207	2	JC4679	vascular endothelial	3.19e-175
2	938	64.6	188	2	JC4680	vascular endothelial	1.15e-117
3	938	25.7	232	2	A41551	vascular endothelial	7.14e-35
4	371	25.6	190	2	A35987	glioma-derived vascul	1.36e-34
5	371	25.6	214	2	A44881	vascular endothelial	1.36e-34
6	367	25.3	190	2	B44881	vascular endothelial	4.94e-34
7	364	25.1	190	2	S52130	vascular endothelial	1.30e-33
8	361	24.9	146	2	S57956	ovine vascular endoth	3.40e-33
9	358	24.7	190	2	B40080	vascular endothelial	8.91e-33
10	353	24.3	120	2	A33787	vascular endothelial	4.43e-32
11	306	21.1	149	2	A41336	placental growth fact	1.35e-25
12	293	20.2	133	2	B45530	vascular endothelial	7.91e-24
13	279	19.2	158	2	A56125	placental growth fact	6.17e-22
14	264	18.2	128	2	I51295	vascular endothelial	6.32e-20
15	189	13.0	225	2	S25097	platelet-derived grow	3.18e-10
16	180	12.4	161	1	I38108	platelet-derived grow	4.12e-09
17	180	12.4	226	1	TVWVSS	PDGF-related transfor	4.12e-09
18	180	12.4	230	1	A55030	platelet-derived grow	4.12e-09
19	180	12.4	241	1	PERHGC	platelet-derived grow	4.12e-09
20	179	12.3	185	2	S53883	hypothetical protein	5.47e-09
21	179	12.3	241	1	PFMSG8	platelet-derived grow	5.47e-09
22	179	12.3	245	1	TVCTSS	platelet-derived grow	5.47e-09
23	175	12.1	166	2	JN0248	platelet-derived grow	1.69e-08

24	175	12.1	419	2	S69207	vascular endothelial	1.69e-08
25	174	12.0	148	2	D49530	16k vascular endothel	2.23e-08
26	171	11.8	198	2	J50735	platelet-derived grow	5.16e-08
27	172	11.8	211	1	PERHGC	platelet-derived grow	3.90e-08
28	165	11.4	197	2	S25096	platelet-derived grow	2.72e-07
29	166	11.4	271	2	A25669	PDF-related transfor	3.07e-07
30	164	11.3	196	2	B28964	platelet-derived grow	3.59e-07
31	163	11.2	200	2	I51551	platelet-derived grow	4.72e-07
32	163	11.2	215	2	S08220	platelet-derived grow	4.72e-07
33	163	11.2	226	2	I51550	platelet-derived grow	4.72e-07
34	161	11.1	196	2	A37359	platelet-derived grow	8.17e-07
35	153	10.5	63	5	1PDGB2	platelet-derived grow	7.18e-06
36	153	10.5	66	5	1PDGAC	platelet-derived grow	7.18e-06
37	153	10.5	68	5	1PDGAC	platelet-derived grow	7.18e-06
38	153	10.5	473	2	S50755	platelet-derived grow	7.18e-06
39	145	10.0	196	2	A48851	hypothetical protein	6.08e-05
40	141	9.7	901	2	A48227	platelet-derived grow	1.74e-04
41	139	9.6	442	2	S50062	cell wall glycoprotei	2.94e-04
42	136	9.4	416	1	SKXIAG	dermal gland protein	6.39e-04
43	137	9.4	474	2	S15921	protein rpx-VT3 - The	4.94e-04
44	136	9.4	699	2	C43674	USA protein - human h	6.39e-04
45	135	9.3	377	2	A48018	mucin 7 precursor, sa	8.27e-04

ALIGNMENTS

RESULT 1
ENTRY JC4679 #type complete
TITLE vascular endothelial growth factor-related factor 186 - mouse
ALTERNATE_NAMES VRF 186 protein, VEGF 186
ORGANISM #formal name Mus musculus #common name house mouse
DATE 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 10-Sep-1997

ACCESSIONS JC4679
REFERENCE JC4679
#authors Townsend, S.; Lagercrantz, J.; Grimmond, S.; Silins, G.;
Nordenskiold, M.; Weber, G.; Hayward, N.
#journal Biochem Biophys. Res. Commun. (1996) 220:922-928
#title Characterization of the murine VEGF-related factor gene.
#accession JC4679
#molecule_type mRNA
#residues 1-207 #label TOM
#cross-references GB:U43836; NID:G1703480; PID:g1314334

COMMENT This factor is a mitogen, that is selective for endothelial cells,
and belongs to a family of growth factors. This transcript is
differentially spliced to produce two major isoforms, vascular
endothelial growth factors 167 and 186.

GENETICS

#gene VRF
#map_position 19
#growth factor

KEYWORDS
FEATURE 1-21
22-207
#domain signal sequence #status predicted #label SIG
#product vascular endothelial growth factor related
factor #status predicted #label VRF
SUMMARY #length 207 #molecular_weight 21914 #checksum 1525

Query Match 90.8%; Score 1319; DB 2; Length 207;
Best Local Similarity 87.0%; Pred. No. 3.19e-175;
Matches 180; Conservative 17; Mismatches 10; Indels 0; Gaps 0;

Db	1	MSPILRLILVALLOLAPVSOFGDPSHQKRVYPIIDVYARATCOPREVVYPLSMEL	60
Oy	1	MSPILRLILVALLOLAPVSOFGDPSHQKRVYPIIDVYARATCOPREVVYPLSMEL	60
Db	61	MGNVYKOLVPCVYORCGCCPDGECPTGHOVMOILMOYPSOIGENSLERS	120
Oy	61	MGNVYKOLVPCVYORCGCCPDGECPTGHOVMOILMOYPSOIGENSLERS	120
Db	61	MGTAKOLVPCVYORCGCCPDGECPTGHOVMOILMOYPSOIGENSLERS	120
Oy	61	MGTAKOLVPCVYORCGCCPDGECPTGHOVMOILMOYPSOIGENSLERS	120
Db	121	OCCEPRKKESAVKPDRAVPAHHRPQSPVGMSTPGASPADIHPTAPGSSARLAP	180
Oy	121	OCCEPRKKESAVKPDRAVPAHHRPQSPVGMSTPGASPADIHPTAPGSSARLAP	180
Db	121	OCCEPRKKESAVKPDRAVPAHHRPQSPVGMSTPGASPADIHPTAPGSSARLAP	180
Oy	121	OCCEPRKKESAVKPDRAVPAHHRPQSPVGMSTPGASPADIHPTAPGSSARLAP	180

 W P O S E R H
 (TW)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Fri Sep 18 13:28:23 1998; Maspar time 7.27 Seconds
 460,975 Million cell updates/sec
 Tabular output not generated.

Title: >US-08-765-588-4
 Description: (1-207) from US08765588.pep
 Perfect Score: 1452
 Sequence: 1 MSPLLRLALLALQLAPAQ.....PGPAAAMDAASVAKGGA 207

Scoring table: PAM 150
 Gap 11

Searched: 131922 segs, 16180660 residues
 Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database:

a-geneseq32
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29

Statistics: Mean 31.715; Variance 158.417; scale 0.200

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1452	100.0	207	19	W00725 Vascular endothelial	5.23e-111
2	1452	100.0	207	21	W04831 Vascular endothelial	5.23e-111
3	1319	90.8	207	21	W04830 Vascular endothelial	1.15e-99
4	1310	90.2	207	19	W00863 Murine VRF186.	6.70e-99
5	1114	76.7	221	23	W07611 Human Vascular endoth	3.11e-82
6	1023	70.5	143	19	W00727 Vascular endothelial	1.61e-74
7	1014	69.8	188	19	W00726 Vascular endothelial	9.33e-74
8	1014	69.8	188	21	W04829 Fibrosarcoma vascular	9.33e-74
9	938	64.6	188	21	W04826 Heart vascular endoth	2.50e-67
10	928	63.9	188	19	W00864 Murine VRF167.	1.75e-66
11	897	61.8	133	21	W04827 Vascular endothelial	7.23e-61
12	861	59.3	195	21	W04828 Heart vascular endoth	7.84e-61
13	749	51.6	101	19	W00728 Vascular endothelial	2.05e-51
14	709	48.8	102	21	W04824 Vascular endothelial	4.59e-48
15	395	27.2	500	18	W00589 SAP-AlaMet-VGEGF121-G1	4.14e-22
16	395	26.8	377	18	W00586 SAP-AlaMet-VGEGF121	1.27e-21
17	389	26.8	506	18	W00588 SAP-AlaMet-VGEGF121(G1	1.27e-21
18	389	26.8	512	18	W00590 SAP-AlaMet-VGEGF121(G1	1.27e-21

19	383	26.4	146	5	R27354	Sequence of vascular
20	383	26.4	146	4	R22348	Alternative form of V
21	383	26.4	595	18	W00595	SAP-GlySer-VGEGF165(G1
22	382	26.3	148	18	R40332	VEGF121 Cys+2.
23	382	26.3	384	18	R94071	SAP(Gly4Ser)VEGF121.
24	382	26.3	399	18	W00587	SAP(Gly4Ser)VEGF121.
25	382	26.3	514	18	R94073	SAP(Gly4Ser)VEGF121(G
26	382	26.3	524	18	W00594	SAP(Gly4Ser)VEGF121(G
27	381	26.2	421	18	W00584	SAP-AlaMet-VGEGF165.
28	381	26.2	588	18	W00592	SAP-AlaMet-VGEGF165-G1
29	381	26.2	594	18	W00591	SAP-AlaMet-VGEGF165(G1
30	381	26.2	600	18	W00593	SAP-AlaMet-VGEGF165(G1
31	379	26.1	147	16	R1075	Human vascular endoth
32	379	26.1	147	18	R94001	VEGF121.
33	378	26.0	121	3	R11385	Human vascular endoth
34	378	26.0	121	7	R42607	Human VEGF-121.
35	377	26.0	546	27	W82334	VEGF/CPG2 fusion prot
36	374	25.8	192	18	R94040	VEGF165 Cys+2.
37	375	25.8	214	4	R22351	Alternative form of V
38	375	25.8	214	5	R27355	Sequence of vascular
39	374	25.8	428	18	R94072	SAP(Gly4Ser)VEGF165.
40	374	25.8	443	18	W00585	SAP(Gly4Ser)VEGF165.
41	374	25.8	598	18	R94074	SAP(Gly4Ser)VEGF165(G
42	374	25.8	612	18	W00596	SAP(Gly4Ser)VEGF165(G
43	373	25.7	215	16	R91077	Human vascular endoth
44	373	25.7	215	1	R05102	Human vascular pernea
45	373	25.7	232	18	R94004	VEGF206.

ALIGNMENTS

RESULT 1
 ID W00725 standard; Protein; 207 AA.
 DF W00725:
 30-NOV-1996 (first entry)



DE Vascular endothelial growth factor-like protein SOM175.
 KW Vascular endothelial growth factor; VEGF; VEGF165; SOM175; neuron;
 OS astroglial proliferation.
 OS Homo sapiens.


PH Key location/Qualifiers
 FT peptide 1..21
 FT /label= sig_peptide

PN W09627007-A1.
 PD 06-SEP-1996.
 PE 23-FEB-1996; AU0094.
 PR 02-MAR-1995; AU-001457.
 PR 20-NOV-1995; AU-006647.
 PR 22-DEC-1995; AU-007274.
 PA (AMRA-) AMRAD OPERATIONS PTY LTD.
 PI Grimmond S, Hayward NK, Larsson C, Nordenskjold M;
 PI Weber G;
 PI WPI; 96-412774/41.
 DR N-PSDB; T33610.

PT New growth factor related to vascular endothelial growth factor -
 PT useful for inducing astroglial proliferation and promoting neuronal
 PT survival.
 PS Claim 11; Page 41; 13pp; English.
 CC Human vascular endothelial growth factor (VEGF)-like polypeptide
 CC (W00725) is capable of inducing the proliferation of vascular
 CC endothelial cells, of interacting with flt-1/fk1-1 receptors,
 CC and of inducing cell migration, cell survival and/or an increase
 CC in intracellular levels of alkaline phosphatase. It shows 33.3%
 CC identity with human VEGF (see also W00724). Splice variants
 CC (W00726-28) of SOM175 have also been identified. Recombinant SOM175
 CC can be produced in host cells transformed with vectors carrying
 CC SOM175 cDNA (see also T33610). It is useful for inducing astroglial
 CC proliferation and for promoting neural survival and/or proliferation.
 SQ Sequence 207 AA.

Query Match 100.0%; Score 1452; DB 19; Length 207;
 Best Local Similarity 100.0%; Pred. No. 5.23e-111;
 Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;




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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on:      Fri Sep 18 13:58:22 1998;      MasPar time 7.36 Seconds
Tabular output not generated.      577.863 Million cell updates/sec

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Title: >US-08-765-588-10
Description: (1-101) from US08765588 pep
Perfect Score: 754
Sequence: 1 MSPILRLRLAALLQLAPAO.....CPDDGLECVPTPGHQVNRQT 101

```

Scoring table: PAM 150
Gap 11

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl6
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp Vertebrate
13:sp_unclassified

Statistics: Mean 38.781; Variance 69.409; scale 0.559

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No
1	749	99.3	207	2	016529	VAGE RELATED FACTOR IS	2.19e-11
2	682	90.5	207	10	064320	VASCULAR ENOTHELIAL G	5.75e-11
3	381	47.9	116	10	035485	VASCULAR ENOTHELIAL G	9.20e-55
4	246	34.0	232	2	016889	VASCULAR ENOTHELIAL G	2.39e-33
5	230	31.8	148	12	042571	VASCULAR ENOTHELIAL G	4.85e-22
6	240	31.8	194	12	042572	VASCULAR ENOTHELIAL G	4.85e-22
7	239	30.4	216	12	091420	VASCULAR ENOTHELIAL G	8.66e-22
8	206	27.3	158	10	063434	PLACENTA GROWTH FACTOR	3.78e-22
9	170	22.5	75	4	018843	VASCULAR ENOTHELIAL G	4.06e-11
10	170	22.5	358	10	P97946	VASCULAR ENOTHELIAL G	4.06e-11
11	170	22.5	415	10	P97953	VASCULAR ENOTHELIAL G	4.06e-11
12	164	21.8	336	10	035251	VASCULAR ENOTHELIAL G	5.58e-11
13	153	20.3	210	4	029613	C-SIS ONCOGENE (PLATEL	6.33e-11
14	150	19.8	185	2	013554	C-SIS PROTO-ONCOGENE (2.26e-11
15	150	19.9	271	11	041483	POLYPROTEIN PRECURSOR	1.31e-07
16	129	17.1	183	10	063740	PGF PROTEIN (FRAGMENT	1.00e-04
17	112	14.9	136	10	035757	VASCULAR ENOTHELIAL G	9.68e-07
18	93	12.3	411	8	038946	GLUTAMATE DEHYDROGENAS	3.75e-07
19	89	11.8	571	9	051763	TS162 DNA.	7.27e-07
20	87	11.5	411	8	004937	MDH GLUTAMATE DEHYDRO	

21	86	11.4	394	9	P66447	EXD6-	VOLTAGE-DEPENDENT CALC	1.01e+00
22	86	11.4	605	2	000304	GLUTAMATE DEHYDROGENAS	1.40e+00	
23	85	11.3	411	8	004872	GLUTAMATE DEHYDROGENAS	1.40e+00	
24	85	11.3	411	8	043260	GLUTAMATE DEHYDROGENAS	1.40e+00	
25	85	11.3	411	8	043871	GLUTAMATE DEHYDROGENAS	1.40e+00	
26	85	11.3	412	8	P93541	GLUTAMATE DEHYDROGENAS	1.40e+00	
27	85	11.3	423	10	P97569	KILLISTATIN	1.40e+00	
28	84	11.1	641	10	008463	FRIZZLED PROTEIN HOMOL	1.93e+00	
29	83	11.0	393	9	064613	(INDIVIDUAL ISOLATE 11	2.65e+00	
30	83	11.0	393	9	064610	MAJOR OUTER MEMBRANE P	2.65e+00	
31	83	11.0	393	9	064612	MAJOR OUTER MEMBRANE P	2.65e+00	
32	83	11.0	393	9	064614	MAJOR OUTER MEMBRANE P	2.65e+00	
33	83	11.0	393	9	046411	(INDIVIDUAL ISOLATE 98	2.65e+00	
34	83	11.0	393	9	064615	MAJOR OUTER MEMBRANE P	2.65e+00	
35	83	11.0	393	9	064609	MAJOR OUTER MEMBRANE P	2.65e+00	
36	83	11.0	394	9	006020	MAJOR OUTER MEMBRANE P	2.65e+00	
37	83	11.0	394	9	046408	MAJOR OUTER MEMBRANE P	2.65e+00	
38	83	11.0	396	9	046406	MAJOR OUTER MEMBRANE P	2.65e+00	
39	83	11.0	722	3	019738	FZEL12.1 (FRAGMENT)	2.65e+00	
40	83	11.0	1031	3	009489	ORANSELLE-TYPE CALCULUM	2.65e+00	
41	83	11.0	4096	2	013337	DNA-DEPENDENT PROTEIN	2.65e+00	
42	83	11.0	4127	2	P78527	DNA-DEPENDENT PROTEIN	2.65e+00	
43	82	10.9	488	11	003832	ENVY POLYPROTEIN (CONTA	3.64e+00	
44	82	10.9	619	10	062309	TELEST NUCLEAR RNA-BIN	3.64e+00	
45	82	10.9	684	2	Q14050	ALPHA-3 TYPE IX COLLAG	3.64e+00	

ALIGNMENTS

ID	RESULT	1	PRELIMINARY;	PRT:	207 AA.
AC	016528				
AC	016528;				
DT	01-NOV-1996	(TREMBLREL. 01. CREATED)			
DT	01-NOV-1996	(TREMBLREL. 01. LAST SEQUENCE UPDATE)			
DT	01-JAN-1998	(TREMBLREL. 05. LAST ANNOTATION UPDATE)			
DE	VEGF RELATED FACTOR ISOFORM VF186	PRECURSOR.			
GN	VEGF OR VEGF-B.				
OS	HOMO SAPIENS (HUMAN).				
OC	ECRAYORNA, METAZOA:	CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	ETHERIA; PRIMATES.				
NC	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-BEAIN;				
RA	GRIMMOND S., LIGERCRANTZ J., DRINKWATER C., SILLIS G., TOMNISON S.,				
RA	POLLACK P., GOTLEY D., CARSON E., RAKAR S., NORDENSKJOLD M., WARD L.				
RA	HAYWARD N., WEBER G.;				
RL	GENOME RES. 6:122-129(1996).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-FIBROSARCOMA HT-1080;				
RC	MEDLINE; 96197355.				
RA	OIOFSSON B.;				
RA	PROC. NATL. ACAD. SCI. U.S.A. 93:2576-2581(1996).				
RL	[3]				
RN	SEQUENCE FROM N.A.				
RP	TISSUE-FIBROSARCOMA HT-1080;				
RC	MEDLINE; 96325041.				
RX	ERIKSSON B., PAJUSOLA K., VON EUDER G., CHILOV D., ALITALO K.,				
RA	OIOFSSON U.;				
RA	J. BIOL. CHEM. 271:19310-19311(1996).				
RL	EMBL; U43368; G1216396; -				
DR	EMBL; U52819; G1488259; -				
DR	PROSITE; PS00249; PDGF; 1.				
KW	SIGNAL.				
FT	SIGNAL.				
FT	CHAIN	1 21	POTENTIAL.		
FT	SEQUENCE	22 207	VEGF RELATED FACTOR ISOFORM VF186.		
SO	SEQUENCE	207 AA; 21602 MW; 18BDP6F1 CRC32;			
	Query Match	99.3%;	Score 749;	DB 2;	Length 207;
	Best Local Similarity	100.0%;	Pred. No. 2.19e-142;		
	Matches 100; Conservative	0;	Mismatches 0;	Indels 0;	Gaps
DB	1 MSPILRLLIALIQLAPAGAVSQPDAPGAGQRKRVYVSMIDVYFRATCPQREYVPLTVEL 60				

 M I S E R I E (TW)

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Msrch.p protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:57:41 1998; Maspar time 4.15 seconds

Tabular output not generated. 610.764 Million cell updates/sec

Title: >US-08-765-588-10
 Description: (1-101) from US08765588.pep
 Perfect Score: 754
 Sequence: 1 MSPLLRLLALQLAPAQ.....CPDDGECVPTGQGVQMOT 101

Scoring table: PAM 150
 Gap 11

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-Prot35
 1:swiss1

Statistics: Mean 40.632; Variance 65.664; scale 0.619

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query length	ID	Description	Pred. No.
1	749	99.3	188	1	VEGF_HUMAN VASCULAR ENDOTHELIAL G	9.02e-157
2	682	90.5	188	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	9.35e-140
3	256	34.0	188	1	VEGF_HUMAN VASCULAR ENDOTHELIAL G	1.71e-35
4	249	33.0	190	1	VEGF_PIG VASCULAR ENDOTHELIAL G	6.68e-34
5	244	32.4	190	1	VEGF_PIG VASCULAR ENDOTHELIAL G	9.07e-33
6	240	31.8	190	1	VEGF_BOVIN VASCULAR ENDOTHELIAL G	7.25e-32
7	240	31.8	214	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	7.25e-32
8	235	31.2	146	1	VEGF_SHEEP VASCULAR ENDOTHELIAL G	9.66e-31
9	232	30.8	133	1	VEGF_ORF2 VASCULAR ENDOTHELIAL G	4.55e-30
10	229	30.4	164	1	VEGF_CAVPO VASCULAR ENDOTHELIAL G	2.13e-29
11	218	28.9	170	1	PIGF_HUMAN PLACENTA GROWTH FACTOR	5.93e-27
12	209	27.7	158	1	PIGF_MOUSE PLACENTA GROWTH FACTOR	5.67e-25
13	172	22.8	148	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	4.73e-17
14	166	22.0	419	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	8.31e-16
15	160	21.2	128	1	VEGF_MOUSE VASCULAR ENDOTHELIAL G	1.42e-14
16	157	20.8	225	1	PDGF_RAT PLATELET-DERIVED GROWTH	5.77e-13
17	153	20.3	245	1	PDGF_FELCA PLATELET-DERIVED GROWTH	3.71e-13
18	152	20.2	241	1	PDGF_MOUSE PLATELET-DERIVED GROWTH	5.89e-12
19	150	19.9	226	1	TSG1_SMSAY PDGF-RELATED TRANSFORM	1.48e-12
20	150	19.9	241	1	PDGF_HUMAN PLATELET-DERIVED GROWTH	1.48e-12
21	149	19.8	241	1	PDGF_SHEEP PLATELET-DERIVED GROWTH	2.35e-12
22	138	18.3	213	1	PDGF_RABBIT PLATELET-DERIVED GROWTH	3.42e-10
23	132	17.5	211	1	PDGF_MOUSE PLATELET-DERIVED GROWTH	4.88e-09

24	131	17.4	204	1	PDGF_RAT PLATELET-DERIVED GROWTH	7.56e-09
25	131	17.4	211	1	PDGF_HUMAN PLATELET-DERIVED GROWTH	7.56e-09
26	130	17.2	226	1	PDGF_XENLA PLATELET-DERIVED GROWTH	1.17e-08
27	91	12.1	411	1	DHE3_VITVI GLUTAMATE DEHYDROGENAS	7.79e-02
28	91	12.1	493	1	ACHE_HUMAN ACETYLCHOLINE RECEPTOR	7.79e-02
29	90	11.9	539	1	L114_CAEEL LIN-14 PROTEIN	1.12e-01
30	88	11.7	598	1	CYSJ_SALTY SULFITE REDUCTASE (NAD	2.27e-01
31	87	11.5	411	1	LTXO_MOUSE PROTEIN-LYSINE 6-OXIDA	3.23e-01
32	86	11.4	567	1	CB2_HUMAN DIHYDROPYRIDINE-SENSIT	4.57e-01
33	84	11.1	916	1	SCRB_LIMPO BETA SCRUBIN	9.09e-01
34	83	11.0	174	1	Y119_HUMAN HYPOHECTICAL Y-CEROS	1.28e+00
35	83	11.0	308	1	KHSE_BRELA HOMOSELINE KINASE (BC	1.28e+00
36	83	11.0	393	1	OMPE_CHLTR MAJOR OUTER MEMBRANE P	1.28e+00
37	83	11.0	393	1	OMPE_CHLTR MAJOR OUTER MEMBRANE P	1.28e+00
38	83	11.0	394	1	OMPA_CHLTR MAJOR OUTER MEMBRANE P	1.28e+00
39	83	11.0	396	1	OMPA_CHLTR MAJOR OUTER MEMBRANE P	1.28e+00
40	83	11.0	397	1	OMPC_CHLTR MAJOR OUTER MEMBRANE P	1.28e+00
41	83	11.0	397	1	OMPN_CHLTR MAJOR OUTER MEMBRANE P	1.28e+00
42	83	11.0	397	1	OMPH_CHLTR MAJOR OUTER MEMBRANE P	1.28e+00
43	83	11.0	399	1	P2X1_RAT P2X PURINOCEPTOR 1 (AT	1.28e+00
44	83	11.0	491	1	ACHE_BOVIN ACETYLCHOLINE RECEPTOR	1.28e+00
45	83	11.0	1110	1	VGLM_INSV M POLYPROTEIN PRECURSOR	1.28e+00

ALIGNMENTS

RESULT ID	1	STANDARD	PRT	188 AA.
AC	P49765;			
DT	01-OCT-1996 (REL. 34, CREATED)			
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)			
DE	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR).			
GN	VEGFB OR VRF.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RK	MEDLINE; 96197355.			
RA	OLIOFSSON B., PAJUSOLA K., KAIPIAINEN A., VON EULER G., JOUKOV V.,			
RA	SAKSELA O., ORPANA A., PETERSSON R.F., ALITALO K., ERIKSSON U.,			
RL	PROC. NATL. ACAD. SCI. U.S.A. 93:2576-2581(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	GRIMMOND S., LAGECRANTZ J., DRINKWATER C., SILLINS G., TOWNSON S.,			
RA	POLLLOCK P., GUTLEY D., CARSON E., RAKAR S., NORDENSKJOLD M.,			
RA	WARD L., HAYWARD N., WEBER G.,			
RL	GENOME RES. 6:122-129(1996).			
CC	-1- FUNCTION: GROWTH FACTOR FOR ENDOTHELIAL CELLS. BINDS HEPARIN.			
CC	-1- SUBUNIT: HOMODIMER. DISULFIDE-LINKED. CAN ALSO FORM HETERODIMER WITH VEGF.			
CC	-1- SUBCELLULAR LOCATION: SECRETED BUT REMAINS ASSOCIATED TO CELLS OR TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN.			
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXCEPT LIVER.			
CC	HIGHEST LEVELS FOUND IN HEART, SKELETAL MUSCLE AND PANCREAS.			
CC	-1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.			
DR	EMBL; U48801; G1234823; -			
DR	EMBL; U43369; G1216398; -			
DR	MTM; 601398; -			
DR	PROSTATE; PS00249; PDGF. 1			
KM	MITOGEN; GROWTH FACTOR; SIGNAL; HEPARIN-BINDING.			
FT	SIGNAL			
FT	CHAIN			
FT	SEQUENCE			
FT	188 AA; 21261 MW; 35EAB904 CRC32;			
Query Match	99.3%; Score 749; DB 1; Length 188;			
Best Local Similarity	100.0%; Pred. No. 9.02e-157;			
Matches	100; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Db	1 MSPLLRLLALQLAPAQVSPDPAGHQRVSMIDVYRATCPREVVPPLVEL 60			

 M I S E R I E (TM)

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MPsrch.p protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:56:46 1998; Maspar time 6.34 Seconds

Tabular output not generated. 582.395 Million cell updates/sec

Title: >US-08-765-588-10
 Description: (1-101) from US08765588.pep
 Perfect Score: 754
 Sequence: 1 MSPLRLRLALALQLAPAO.....CPDDGLECVPTGQHOVRMOT 101

Scoring table: PAM 150
 Gap 11

Searched: 120441 segs, 36531193 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: plr56
 1:plr1 2:plr2 3:plr3 4:plr4 5:nrl3d

Statistics: Mean 38.722; Variance 77.276; scale 0.501

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	682	90.5	188	2	JC4680	9.95e-114
2	682	90.5	207	2	UC4679	9.95e-114
3	256	30.0	232	2	A41551	8.21e-29
4	249	33.0	190	2	S52130	1.65e-27
5	244	32.4	190	2	A35987	1.40e-26
6	240	31.8	190	2	B44881	7.68e-26
7	240	31.8	190	2	B40080	7.68e-26
8	240	31.8	214	2	A44881	7.68e-26
9	235	31.2	146	2	S57956	6.41e-25
10	231	30.6	133	2	B49530	3.48e-24
11	227	30.1	120	2	A33787	1.88e-23
12	218	28.9	149	2	A41236	8.17e-22
13	218	28.9	158	2	A56125	1.19e-19
14	172	22.3	148	2	D49530	1.13e-13
15	166	22.0	419	2	S69207	1.20e-12
16	160	21.2	128	2	I51295	1.24e-11
17	157	20.8	225	2	S25097	3.96e-11
18	153	20.3	245	1	TYC7CS	1.84e-10
19	152	20.2	241	1	PFMSGB	2.70e-10
20	150	19.9	161	2	I38108	5.79e-10
21	150	19.9	185	2	S58383	5.79e-10
22	150	19.9	226	1	TVWVSS	5.79e-10
23	150	19.9	230	2	A55030	5.79e-10

24	150	19.9	241	1	PRHUG2	platelet-derived grow	5.79e-10
25	150	19.9	271	2	A25669	PGF-related transfor	5.79e-10
26	138	18.3	166	2	JN0248	platelet-derived grow	5.24e-08
27	138	18.3	198	2	J50735	platelet-derived grow	5.24e-08
28	133	17.6	63	5	1PDG82	platelet-derived grow	3.30e-07
29	133	17.6	66	5	1PDG82	platelet-derived grow	3.30e-07
30	133	17.6	68	5	1PDG82	platelet-derived grow	3.30e-07
31	131	17.4	196	2	B28964	platelet-derived grow	6.84e-07
32	131	17.4	197	2	S25096	platelet-derived grow	6.84e-07
33	131	17.4	211	1	PRHUG1	platelet-derived grow	6.84e-07
34	130	17.2	200	2	I51551	platelet-derived grow	9.83e-07
35	130	17.2	215	2	S08220	platelet-derived grow	9.83e-07
36	130	17.2	226	2	I51550	platelet-derived grow	9.83e-07
37	128	17.0	196	2	A37359	platelet-derived grow	2.02e-06
38	112	14.9	196	2	A48851	platelet-derived grow	5.56e-04
39	91	12.1	36	2	A60706	vascular endothelial	5.05e-01
40	91	12.1	411	2	S54797	glutamate dehydrogena	5.05e-01
41	91	12.1	493	2	S34775	nicotinic acetylcholi	5.05e-01
42	90	11.9	537	2	B40581	embryonic nuclear pro	6.84e-01
43	90	11.9	539	2	A40581	embryonic nuclear pro	6.84e-01
44	88	11.7	599	2	A34231	sulfite reductase (NA	1.25e+00
45	88	11.7	604	2	A42044	beta subunit of L-tyr	1.25e+00

ALIGNMENTS

RESULT ENTRY	1	JC4680	#type complete
TITLE	vascular endothelial growth factor-related factor 167 - mouse		
ALTERNATE_NAMES	VRF 167 protein		
ORGANISM	#formal_name Mus musculus #common_name house mouse		
DATE	10-MAY-1996 #sequence_revision 19-Jul-1996 #text_change 10-Sep-1997		

ACCESSIONS REFERENCE	JC4680	JC4679
#authors	Townson, S.; Lagercrantz, J.; Grimmond, S.; Sillins, G.; Nordenskjold, M.; Weber, G.; Hayward, N.	Biochem. Biophys. Res. Commun. (1996) 220:922-928
#journal	Characterization of the murine VEGF-related factor gene.	
#title	JC4680	
#accession	#molecule_type mRNA	
#residues	1-188 #label TOM	
#cross-references	GB:U43837; NID:91314335; PID:91314336	

COMMENT This factor is a mitogen, that is selective for endothelial cells, and belongs to a family of growth factor. This transcript is differentially spliced to produce two major isoforms, vascular endothelial growth factors 167 and VEGF 186.

GENETICS

#gene	vrf
#map_position	137/72
#introns	
FEATURE	
1-21	#domain signal sequence #status predicted #label SIG
22-188	#product vascular endothelial growth factor-related factor #status predicted #label MAT
SUMMARY	#length 188 #molecular_weight 21442 #checksum 5681

Query Match	90.5%	Score 682;	DB 2;	Length 188;
Best Local Similarity	87.0%	Pred. No. 9.95e-114;		
Matches	87;	Conservative	8;	Mismatches 5;
			Indels	0;
			Gaps	0;

DB	1	MSPLRLRLALALQLAPAOVSQFPGSPSHQKRVVWIDVYAATQCPRVVPLSMEL	60
OY	1	MSPLRLRLALALQLAPAOVSQFPGSPSHQKRVVWIDVYAATQCPRVVPLSMEL	60

DB	61	MGNVKKOLVPSCVTVQRCGCCPDGECVPTGQHOVRMOT	100
OY	61 <th>MGNVKKOLVPSCVTVQRCGCCPDGECVPTGQHOVRMOT</th> <th>100</th>	MGNVKKOLVPSCVTVQRCGCCPDGECVPTGQHOVRMOT	100

RESULT ENTRY	2	JC4679	#type complete
TITLE	vascular endothelial growth factor-related factor 186 - mouse		

M P O E N E H I
(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 13:55:32 1998; MasPar time 4.82 seconds

Tabular output not generated. 339,293 Million cell updates/sec

Title: >US-08-765-588-10
Description: (1-101) from US08765588.pep
Perfect Score: 754
Sequence: 1 MSPILRLILALILQALAPAQ.....CPDDGLECVPTGQHOVMQT 101

Scoring table:
Gap 11
PAM 150

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 28.818; Variance 119.725; scale 0.241

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	754	100.0	101	19	W00728 Vascular endothelial	8,296-64
2	749	99.3	143	19	W00727 Vascular endothelial	2,666-63
3	749	99.3	188	21	W04829 Fibrosarcoma vascular	2,666-63
4	749	99.3	187	19	W00726 Vascular endothelial	2,666-63
5	749	99.3	207	21	W04831 Vascular endothelial	2,666-63
6	749	99.3	207	21	W00725 Vascular endothelial	2,666-63
7	682	90.5	133	21	W04828 Vascular endothelial	1,546-56
8	682	90.5	188	19	W00826 Heart vascular endoth	1,546-56
9	682	90.5	188	19	W00864 Murine VEGF167	1,546-56
10	682	90.5	195	21	W04827 Heart vascular endoth	1,546-56
11	682	90.5	207	21	W04830 Murine VEGF186	1,546-56
12	682	90.5	207	19	W00863 Vascular endothelial	1,546-56
13	625	82.9	221	23	W07611 Human vascular endoth	8,386-51
14	494	65.5	102	21	W04824 Vascular endothelial	1,046-37
15	268	35.3	595	18	W00595 SAP-GLYser-VEGF165(G1	1,216-15
16	266	35.3	377	18	SAP-ALamet-VEGF121	1,886-15
17	266	35.3	421	18	SAP-ALamet-VEGF165	1,886-15
18	266	35.3	500	18	SAP-ALamet-VEGF121-G1	1,886-15

19	266	35.3	506	18	W00588 SAP-ALamet-VEGF121(G1	1,886-15
20	266	35.3	512	18	W00590 SAP-ALamet-VEGF121(G1	1,886-15
21	266	35.3	588	18	W00592 SAP-ALamet-VEGF165(G1	1,886-15
22	266	35.3	594	18	W00591 SAP-ALamet-VEGF165(G1	1,886-15
23	266	35.3	600	18	W00593 SAP-ALamet-VEGF165(G1	1,886-15
24	259	34.4	148	18	R94032 VEGF121 Cys+2	8,656-15
25	259	34.4	192	18	R94040 VEGF165 Cys+2	8,656-15
26	259	34.4	384	18	R94071 SAP(G1Y4Ser)VEGF121	8,656-15
27	259	34.4	399	18	W00587 SAP(G1Y4Ser)VEGF121	8,656-15
28	259	34.4	428	18	R94072 SAP(G1Y4Ser)VEGF165	8,656-15
29	259	34.4	443	18	W00585 SAP(G1Y4Ser)VEGF165	8,656-15
30	259	34.4	514	18	R94073 SAP(G1Y4Ser)VEGF121(G	8,656-15
31	259	34.4	524	18	W00594 SAP(G1Y4Ser)VEGF121(G	8,656-15
32	259	34.4	598	18	R94074 SAP(G1Y4Ser)VEGF165(G	8,656-15
33	259	34.4	612	18	W00596 SAP(G1Y4Ser)2VEGF165	8,656-15
34	256	34.0	191	27	W38242 Vascular endothelial	1,666-14
35	256	34.0	191	16	R91076 Human vascular endoth	1,666-14
36	256	34.0	191	19	W00724 Vascular endothelial	1,666-14
37	256	34.0	191	2	R08002 Human vascular endoth	1,666-14
38	256	34.0	215	16	R94003 Human vascular endoth	1,666-14
39	256	34.0	215	16	R91077 Human vascular endoth	1,666-14
40	256	34.0	215	1	R05102 Human vascular permea	1,666-14
41	256	34.0	232	18	R94004 VEGF206	1,666-14
42	256	34.0	232	16	R91078 Human vascular endoth	1,666-14
43	256	34.0	461	18	W00583 VEGF165-ALamet-SAP	1,666-14
44	256	34.0	546	27	W38234 VEGF/CPG2 fusion prot	1,666-14
45	256	34.0	592	27	W38233 VEGF/CPG2 fusion prot	1,666-14

ALIGNMENTS

1
ID W00728 standard: Protein; 101 AA.
AC W00728:

DE 30-NOV-1996 (first entry)
DE Vascular endothelial growth factor-like protein SOM175-e4.
KW Vascular endothelial growth factor; VEGF; SOM175-e4; neuron;
KW astroglial proliferation.
OS Homo sapiens.

FT Key Location/Qualifiers
FT peptide 1..21
FT /label= sig_peptide

PN W09627007-A1.

PD 06-SEP-1996.

PE 22-FEB-1996; AU0094.

PR 02-MAR-1995; AU-001457.

PR 20-NOV-1995; AU-006647.

PA 22-DEC-1995; AU-007274.
(AMRA-) AMRAD OPERATIONS PTY LTD.

PI Grimmond S, Hayward NK, Larsson C, Nordenskjold M;
PI Weber G;

DR WPI: 96-412774/41.

DR N-PSDB: T33613.

PT New growth factor related to vascular endothelial growth factor -
PT useful for inducing astroglial proliferation and promoting neuronal

PT survival

PS Claim 14; Page 48; 113pp; English.

CC Splice variants (W00726-28) of the human vascular endothelial growth

CC factor-like polypeptide SOM175 (see also W00725) are products of

CC cDNA clones (see also T33611-13) respectively lacking exon 6, exons

CC 6+7, and exon 4 of the SOM175 gene (see also T33610). They show at

CC least 1 of the properties of SOM175 including the ability to induce

CC proliferation of vascular endothelial cells, to interact with

CC IL-1/ILK-1 receptors, and to induce cell migration, cell survival

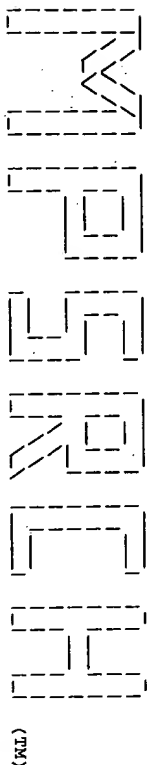
CC and/or an increase in intracellular levels of alkaline phosphatase.

CC Recombinant SOM175 proteins can be used to induce astroglial

CC proliferation and to promote neural survival and/or proliferation.

CC Sequence 101 AA;

Query Match 100.0%; Score 754; DB 19; Length 101;
Best Local Similarity 100.0%; Pred. No. 8,296-64;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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MSPRCH_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Sep 18 14:00:02 1998; Maspar time 7.25 Seconds

Tabular output not generated.

Title: >US-08-765-588-10
Description: (1-101) from US08765588.pep
Perfect Score: 754
Sequence: 1 MSPRLRLALLAQLAPAQ.....CPDGLCVCPTGQHVMQT 101

Scoring table: PAM 150
Gap 11

Searched: 288199 seqs, 31643258 residues

Post-processing: Minimum Match 08
Listing first 45 summaries

Database: a-pending
1:P9 2:U060 3:U7 4:U080 5:U081 6:U082 7:U083 8:U084 9:U085
10:U086 11:U087 12:U088 13:U089 14:U090 15:U091 16:U092
17:U093 18:U094 19:U095 20:U096

Statistics: Mean 28.480; Variance 119.199; scale 0.239

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	749	99.3	188	10	US-	Sequence 56, Applicati	1.35e-62
2	749	99.3	188	9	US-	Sequence 11, Applicati	1.35e-62
3	749	99.3	188	10	US-	Sequence 11, Applicati	1.35e-62
4	749	99.3	188	10	US-	Sequence 11, Applicati	1.35e-62
5	749	99.3	188	11	US-	Sequence 57, Applicati	1.35e-62
6	749	99.3	188	9	US-	Sequence 11, Applicati	1.35e-62
7	749	99.3	188	9	US-	Sequence 11, Applicati	1.35e-62
8	749	99.3	188	8	US-	Sequence 11, Applicati	1.35e-62
9	749	99.3	206	12	US-	Sequence 2, Applicatio	1.35e-62
10	749	99.3	207	9	US-	Sequence 15, Applicati	1.35e-62
11	749	99.3	207	10	US-	Sequence 15, Applicati	1.35e-62
12	749	99.3	207	10	US-	Sequence 15, Applicati	1.35e-62
13	749	99.3	207	10	US-	Sequence 15, Applicati	1.35e-62
14	749	99.3	207	9	US-	Sequence 15, Applicati	1.35e-62
15	685	90.8	188	12	US-	Sequence 1, Applicatio	3.51e-56
16	682	90.5	133	8	US-	Sequence 9, Applicatio	7.02e-56
17	682	90.5	133	8	US-	Sequence 9, Applicatio	7.02e-56
18	682	90.5	133	9	US-	Sequence 9, Applicatio	7.02e-56
19	682	90.5	133	10	US-	Sequence 9, Applicatio	7.02e-56
20	682	90.5	133	10	US-	Sequence 9, Applicatio	7.02e-56
21	682	90.5	133	9	US-	Sequence 9, Applicatio	7.02e-56

22	682	90.5	133	9	US-	Sequence 9, Applicatio	7.02e-56
23	682	90.5	188	8	US-	Sequence 5, Applicatio	7.02e-56
24	682	90.5	188	8	US-	Sequence 5, Applicatio	7.02e-56
25	682	90.5	188	10	US-	Sequence 5, Applicatio	7.02e-56
26	682	90.5	188	9	US-	Sequence 5, Applicatio	7.02e-56
27	682	90.5	188	10	US-	Sequence 5, Applicatio	7.02e-56
28	682	90.5	188	9	US-	Sequence 5, Applicatio	7.02e-56
29	682	90.5	188	9	US-	Sequence 5, Applicatio	7.02e-56
30	682	90.5	195	8	US-	Sequence 7, Applicatio	7.02e-56
31	682	90.5	195	10	US-	Sequence 7, Applicatio	7.02e-56
32	682	90.5	195	9	US-	Sequence 7, Applicatio	7.02e-56
33	682	90.5	195	10	US-	Sequence 7, Applicatio	7.02e-56
34	682	90.5	195	9	US-	Sequence 7, Applicatio	7.02e-56
35	682	90.5	195	8	US-	Sequence 7, Applicatio	7.02e-56
36	682	90.5	195	9	US-	Sequence 7, Applicatio	7.02e-56
37	680	90.2	207	9	US-	Sequence 13, Applicati	1.11e-55
38	680	90.2	207	10	US-	Sequence 13, Applicati	1.11e-55
39	680	90.2	207	9	US-	Sequence 13, Applicati	1.11e-55
40	680	90.2	207	10	US-	Sequence 13, Applicati	1.11e-55
41	680	90.2	207	9	US-	Sequence 13, Applicati	1.11e-55
42	625	82.9	221	8	US-	Sequence 2, Applicatio	3.49e-50
43	625	82.9	221	14	US-	Sequence 2, Applicatio	3.49e-50
44	625	82.9	221	8	US-	Sequence 2, Applicatio	3.49e-50
45	625	82.9	221	12	US-	Sequence 5, Applicatio	3.49e-50

ALIGNMENTS

Sequence 1
US-08-671-573B-56 STANDARD; PRT; 188 AA.
xxxxxx

Sequence 56, Application US/08671573B

Sequence 56, Application US/08671573B

GENERAL INFORMATION:

APPLICANT: Allitalo, Karl

TITLE OF INVENTION: Receptor Ligand

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borum

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/671,573B

FILING DATE: 28-JUN-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/601,132

FILING DATE: 14-FEB-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/585,895

FILING DATE: 12-JAN-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/510,133

FILING DATE: 01-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Gass, David A.

REGISTRATION NUMBER: 38,153

REFERENCE/DOCKET NUMBER: 28967/33348

TELECOMMUNICATION INFORMATION:

(JL)

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protein - protein database search, using Smith-Waterman algorithm

Fri Sep 18 13:59:37 1998; MASPar time 1.79 Seconds

put not generated

>US-08-765-588-10

ce: 754

le: PAM 150

77021 seqs, 7058996 residues

Listing first 45 summaries

a-issued

Mean 26.807; Variance 113.192; scale 0.237

No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed derived by analysis of the total score distribution.

SUMMARIES

Query	Match	Length	DB	ID	Description	Pred. No.	
42	99.3	188	1	US-08-469-	Sequence 11, Applicati	3.54e-63	
89	90.5	133	1	US-08-469-	Sequence 9, Applicatio	1.67e-56	
82	90.5	188	1	US-08-469-	Sequence 5, Applicatio	1.67e-56	
82	90.5	195	1	US-08-469-	Sequence 7, Applicatio	1.67e-56	
94	65.5	102	1	US-08-469-	Sequence 2, Applicatio	6.54e-38	
94	65.5	102	1	US-08-469-	Sequence 7, Applicatio	1.34e-15	
63	34.9	215	3	5219739-22	Patent No. 5219739.	1.67e-15	
37	34.7	231	2	PCR-US96-0	Sequence 10, Applicati	6.12e-15	
36	34.0	191	3	5332671-4	Patent No. 5332671.	6.12e-15	
256	34.0	214	3	5240848-11	Patent No. 5240848.	6.12e-15	
256	34.0	215	3	5240848-7	Patent No. 5240848.	6.12e-15	
255	33.8	121	3	5219739-20	Patent No. 5219739.	7.60e-15	
255	33.8	121	3	5194596-19	Patent No. 5194596.	7.60e-15	
255	33.8	165	3	5219739-19	Patent No. 5194596.	7.60e-15	
255	33.8	165	3	5194596-18	Patent No. 5194596.	7.60e-15	
240	31.8	190	3	5332671-3	Patent No. 5332671.	1.93e-13	
234	31.0	189	1	US-08-469-	Sequence 15, Applicati	6.99e-13	
227	30.1	120	3	5194596-9	Patent No. 5194596.	3.13e-12	
18	221	120	3	5219739-9	Patent No. 5219739.	3.13e-12	
19	227	164	3	5219739-17	Patent No. 5219739.	3.13e-12	
20	227	164	3	5219739-18	Patent No. 5219739.	3.13e-12	
21	227	164	3	5194596-17	Patent No. 5194596.	3.13e-12	
22	218	149	1	US-08-469-	Sequence 14, Applicati	2.13e-11	
23	166	22.0	419	2	PCR-US96-0	Sequence 2, Applicatio	1.15e-06

45	132	17.5	271	3	5175255-1	Sequence 12, Applicant Patent No. 5175255.	1.10e-03
44	132	17.6	196	1	US-08-469	Sequence 12, Applicant Patent No. 5175255.	1.10e-03
43	133	17.5	256	3	5175255-9	Sequence 1, Applicant Patent No. 5175255.	3.00e-05
42	150	19.9	282	1	US-08-445	Sequence 1, Applicant Patent No. 5175255.	3.00e-05
41	150	19.9	241	3	PCT-US96-0	Sequence 1, Applicant Patent No. 5175255.	3.00e-05
40	150	19.9	241	1	US-08-367	Sequence 4, Applicant Patent No. 5175255.	3.00e-05
39	150	19.9	241	1	US-08-367	Sequence 4, Applicant Patent No. 5175255.	3.00e-05
38	150	19.9	241	3	5219739-15	Sequence 1, Applicant Patent No. 5219739.	3.00e-05
37	150	19.9	241	3	5175255-2	Sequence 1, Applicant Patent No. 5175255.	3.00e-05
36	150	19.9	241	3	5194596-15	Sequence 1, Applicant Patent No. 5194596.	3.00e-05
35	150	19.9	226	3	5498600-2	Sequence 1, Applicant Patent No. 5498600.	3.00e-05
34	150	19.9	220	3	5175255-4	Sequence 1, Applicant Patent No. 5175255.	3.00e-05
33	150	19.9	160	1	US-08-094	Sequence 1, Applicant Patent No. 5428135.	3.00e-05
32	150	19.9	129	3	5428135-2	Sequence 18, Applicant Patent No. 5428135.	3.00e-05
31	150	19.9	109	2	PCT-US91-0	Sequence 1, Applicant Patent No. 5428135.	3.00e-05
30	150	19.9	109	2	US-08-094	Sequence 1, Applicant Patent No. 5428135.	3.00e-05
29	150	19.9	109	2	PCT-US93-0	Sequence 1, Applicant Patent No. 5428135.	3.00e-05
28	150	19.9	109	1	US-08-094	Sequence 4, Applicant Patent No. 5498600.	3.00e-05
27	150	19.9	109	3	5498600-3	Sequence 13, Applicant Patent No. 5498600.	3.00e-05
26	152	20.2	241	1	US-08-469	Sequence 13, Applicant Patent No. 5498600.	3.00e-05
25	152	20.2	109	1	US-08-094	Sequence 3, Applicant Patent No. 5498600.	3.00e-05
24	152	20.2	109	1	US-08-094	Sequence 5, Applicant Patent No. 5498600.	3.00e-05

ALIGNMENTS

ID RESULT 1
 XX US-08-469-427A-11 STANDARD; PRT; 188 AA.
 XX xxxxxx
 XX
 DE Sequence 11, Application US/08469427A
 CC
 CC Sequence 11, Application US/08469427A
 CC Patent No. 5607918
 CC GENERAL INFORMATION:
 CC APPLICANT: Eriksson, Ulf
 CC APPLICANT: Olofsson, Birgitta
 CC APPLICANT: Alltalo, Kari
 CC APPLICANT: Pajusola, Katari
 CC TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
 CC TITLE OF INVENTION: DNA CODING THEREFOR
 CC NUMBER OF SEQUENCES: 17
 CC CORRESPONDENCE ADDRESSES:
 CC ADDRESSEE: Evanson, McKeown, Edwards & Lenahan
 CC STREET: 1200 G Street, N.W., Suite 700
 CC CITY: Washington
 CC STATE: DC
 CC ZIP: 20005
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
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 CC FILING DATE: 06-JUN-1995
 CC CLASSIFICATION: 435
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/397,651
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 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 188 amino acids